

FIGURE 1A

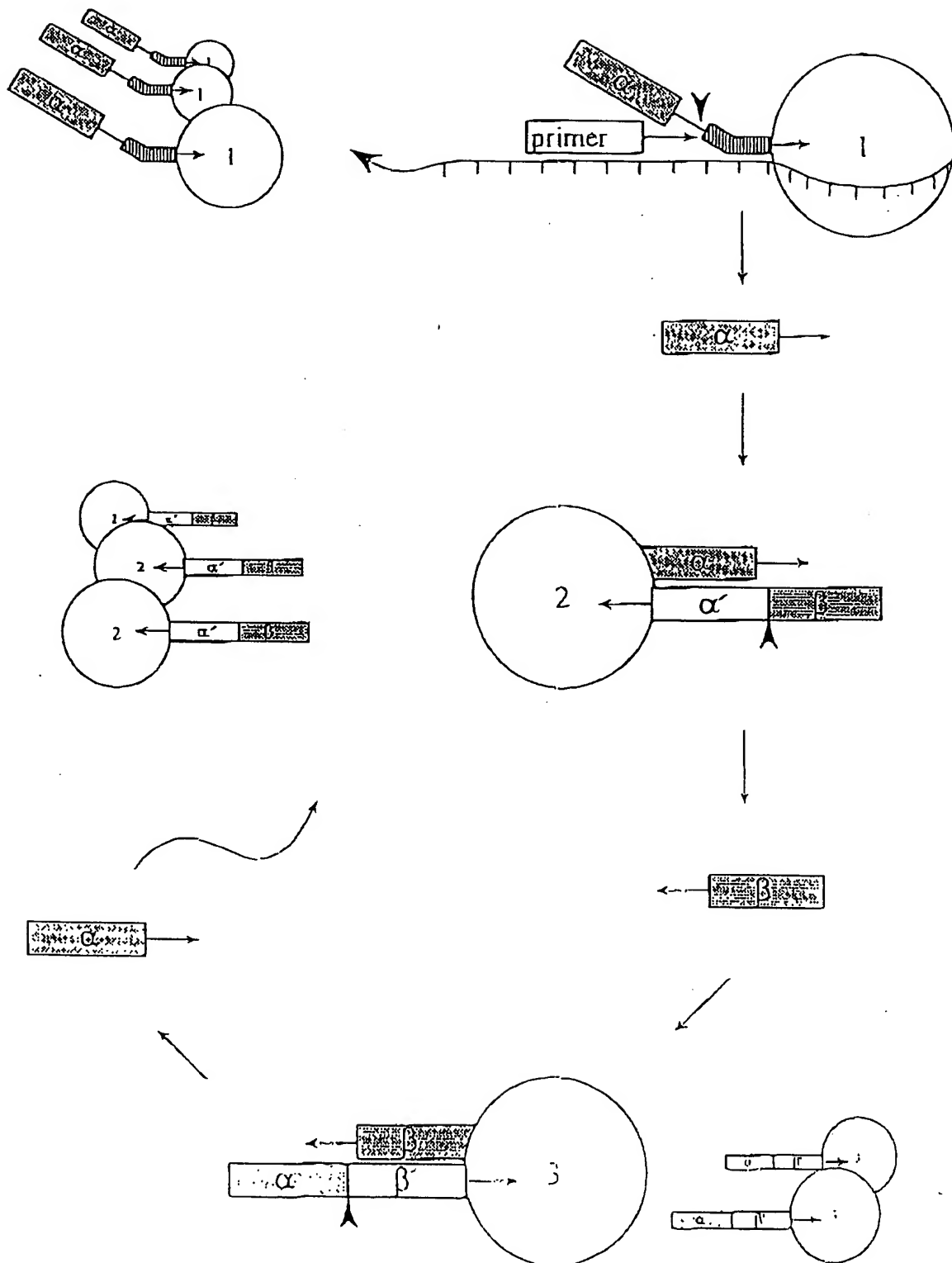
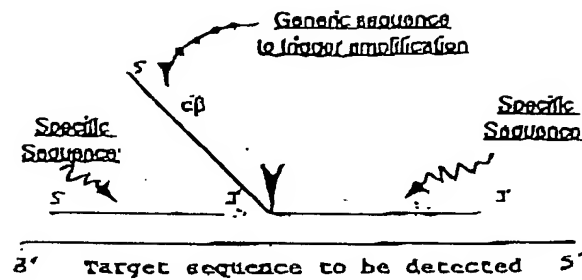


FIGURE 1B

PART ONE: TRIGGER REACTION



PART TWO: DETECTION REACTION

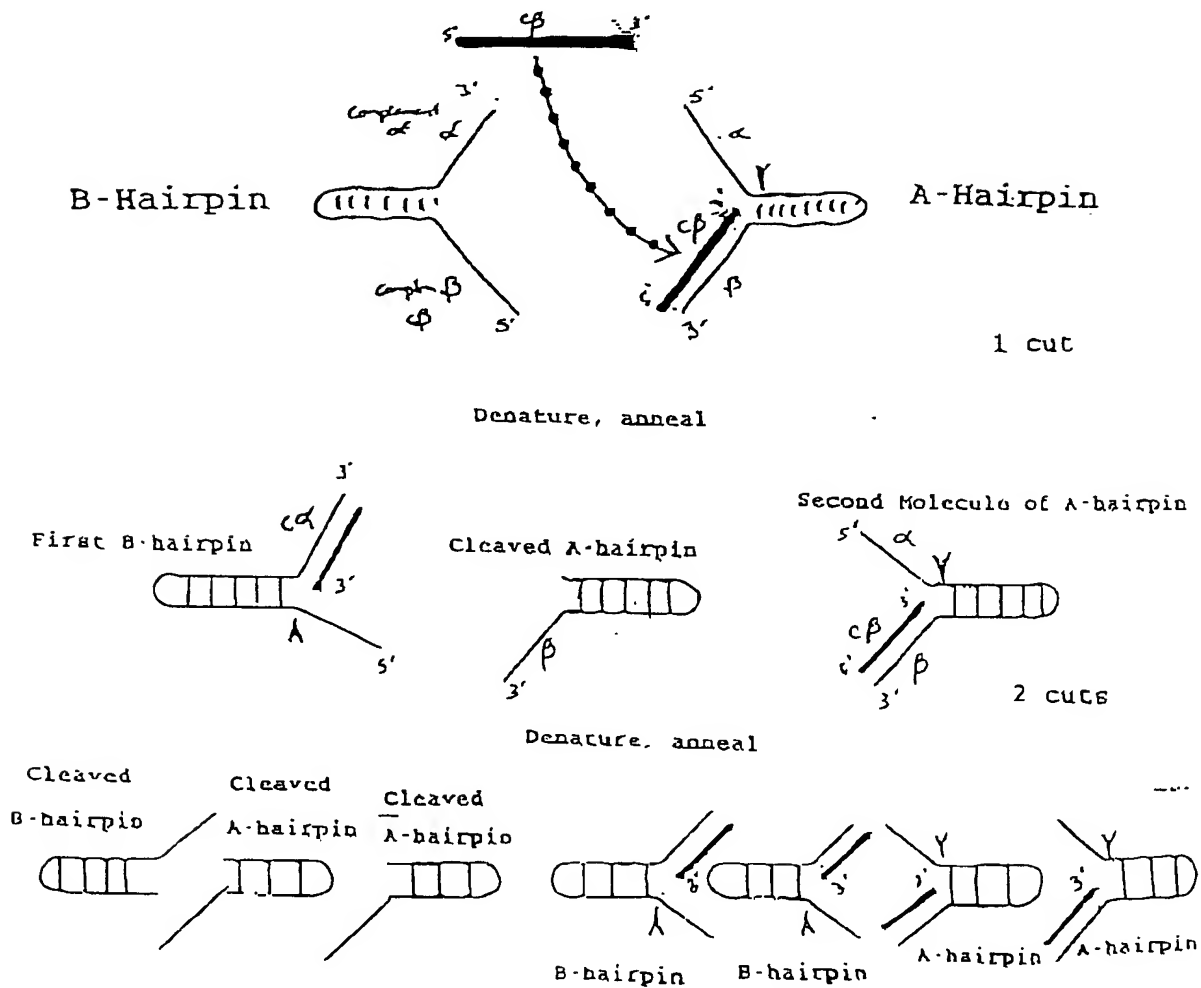


FIGURE 2 (con'd)

MAJORITY (SEQ ID NO:7)	CGACCCCGACGACCTXCTGCCACCGCTGCCCAAGCGCGGAAAGGAGCGGTACGAGGTGGCGATCGCTC	
DNAPTAAO (SEQ ID NO:1)C.....G.....C.....C.....	417
DNAPTFL (SEQ ID NO:2)	I.....G.....CG.....	414
DNAPTHH (SEQ ID NO:3)T..G.....	420
MAJORITY	ACCGCCGACCGCGGAGCTCIACGAGCICCTTTCGACCGGCAICGGCGTCCTCCACCCCGAGGGTACCTCA	
DNAPTAAOAAA.....T.....CA.....	487
DNAPTFL	..T.....A.....G.....G.....A.....T.....G.....	484
DNAPTHHA...G...G.....G.....CC.....	490
MAJORITY	TCACCCCGCGCGCTTTCGAGAACTACCGCGCTGACCGCGGAGCACTGGGTGACTACCGCGCGCGCTCGG	
DNAPTAAOC.....A.....C.....C.....CC.....A.....	557
DNAPTFLAC.....C.....C.....	554
DNAPTHHA.....C.....C.....T...C.....C..T...S60	
MAJORITY	CGCGGACCCCTCCGACAACTCCCGCGGGTCAADGGCATCGGGGAAAGAACCGCCGCAAGCTCCCTCXAG	
DNAPTAAO	C.....GAG.....T.....O...DAG.....T...CG...	627
DNAPTFLG..I...A.....G.....A...G...A...CGG	624
DNAPTHHT.....TC.....A...	630
MAJORITY	GAGTCGGCGGACCGCTGGAAACCTCCCTCAAGAACCTCCGACCGCGTCAACCCCGC...-CXTCCCGGACAGAGA	
DNAPTAAOCG.....CC.....A.....	694
DNAPTFLI...C...C.....A.....T...T...G.....C	691
DNAPTHHA.....A.....A...AAA..C.....	700

4

MAJORITY	(SEQ ID NO:7)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464
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FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	CGCCGXCICCTCGCCCAAGGACCTGGCCGCTTTCGCCCGTCAGCGGAGGCGGCTCXTCGCCCGGCGGACG	
ONAPTAO	(SEQ ID NO:1)C..T.....A.....AC.....C.....A.....T..C.....CC.....C.....	1111
ONAPTR	(SEQ ID NO:2)AA.....C.....G.....C.....C.....T..C.....A..A.....	1120
ONAPTH	(SEQ ID NO:3)C.....C.....C.....C.....T..C.....G..A.....G.....	
MAJORITY		ACCCCA1GCTGCTGGGCTAGCTGCTGGACCCCTCCAACACGACCCCGGAGCGGGGTGGCCCGGCGGCTACGG	
ONAPTAO	T.....	1184
ONAPTR	T.....T.....	1181
ONAPTH	T.....G.....	1190
MAJORITY		CGCCGAGTGGACGCGGACGAXCGCGGCGGAGCGCGGCTCGTXXTCGAGAGGCTCTTCGXGAAGCTXXXGGAG	
ONAPTAO	G.....G.....GC.....T.....GC.....G.....G.....G.....	1254
ONAPTR	T.....A.....GC.....GC.....C..G.....A..G.....AAA.....	1251
ONAPTH	C..C..CGG..C.....C..G.....CAT..G.....CGT..A.....	1260
MAJORITY		CGCCCTTGCAGCGGCGGACGAGGCTGCTTGGCTTTACCCAGGAGCTCGAGAGACGCGGCTTTCGCCCGGCTCGCTCG	
ONAPTAO		A..G.....A.....A..A..AC..C..G.....G.....G.....GCT.....	1324
ONAPTR	C.....A.....C.....C.....C.....A.....C.....G.....G.....	1321
ONAPTH	C.....A.....C.....C.....C.....A.....C.....C.....G.....	1330
MAJORITY		CCACACA1GGAGCGCGGCGGCGGTXCGGCTGGACGCTGGGCTAGCTCGAGCGGCGCTXTCGCTGGAGCTGGCGGGA	
ONAPTAO	G..C.....G.....T.....AG.....T..G.....C.....	1394
ONAPTR	G.....C.....C.....C.....C.....C.....A..C.....	1391
ONAPTH	C.....A.....C.....C.....T.....T.....C..I.....	1400

FIGURE 2 (cont'd)

MAJORITY	(SEQ ID NO:7)	GGAGATCCCGCGGCGTCCAGGCAACAGGCTCTCCCGCTCCCGCGCGCACCCCTTCAACCTCAACTCCCGCGGAC	
ONADP1A0	(SEQ ID NO:1)GC.....GC.....	1464
ONADP1R	(SEQ ID NO:2)CG.....AC.....G.....	1461
ONADP1H	(SEQ ID NO:3)T.....G.....	1462
MAJORITY		CAGC1CGAARAGCGTGC1CTT1GACGAGCTXGCGCGCTTCCCGCGCATCGCGCAAGACGCGAAGACXCGGCAAGC	
ONADP1A0	G.....A.....	1534
ONADP1R	GC.....G.....C.....G.....T.....	1531
ONADP1H	TA.....T.....G.....G.....C.....A.....	1540
MAJORITY		GGTCCACGACGCGCGCGCGTGC1CGAGCGCGCTXCGXGAGCGCGCACCGCCATCGTGGAGAAAGATCC1CGAC1A	
ONADP1A0	G.....C.....C.....G.....	1604
ONADP1R	T.....G.....A.....	1601
ONADP1H	G.....A.....G.....	1610
MAJORITY		CGCGGAGGTCACCAAGCTCAAGAAACACCTACATXGACGCGCGTGGCXGCGCTGCTCCACCGCCAGCGCGCGC	
ONADP1A0	G.....G.....T.....C.....A.....	1617
ONADP1R	A.....A.....C.....C.....G.....	1620
ONADP1H	G.....G.....C.....AAG.....G.....	1680
MAJORITY		CCCC1CCACACCGCGCT1CAACCCACACCGCGCCACCGCGCCACCGCGCT1AGTAGCTCCGACCGCCCAACCTCC	
ONADP1A0	A.....A.....	1744
ONADP1R	G.....C.....TCC.....	1741
ONADP1H	G.....	1750

FIGURE 2 (cont'd)

MAJORITY (SEQ ID NO:7)	AGCTTCCCCCAAGCTCCGGCCCTCCATTCAGAAACACCCCTCCAGGAGCCGACGCGGGCTACCTCCAGA	2184
ONAPTAD (SEQ ID NO:1)	2184
DNAPTTR (SEQ ID NO:2)A.....GG.....C.....C.....C.....T.....	2184
DNAPTTH (SEQ ID NO:3)A.....A.....A.....G.....A.....A.....A.....	2177
MAJORITY	CCCTCTTCCCGCCCGCCCTACCTCCCGGAGCTCAACGCGCCGCTCAAGAGGCTCGCGGACGCGCGCGCA	
ONAPTADC.....A.....AG.C.....C.....	2234
DNAPTTRT.....I.....C.....C.....	2231
DNAPTTHAA.AA.....CA.....C.....	2240
MAJORITY	CGCCATCGCCCTTCAACATCGCCGCTCCAGCGCCAGCGCCGCGGAGCTCATCAAGCTCGCCATCGTCAAGCTC	
ONAPTAD	2304
DNAPTTRG.....T.....C.....T.....	2301
DNAPTTHC.....C.....C.....C.....	2310
MAJORITY	TTCCCGCCGCTXCAGGAAATCGCGCCGAGGATGCTCCIXCAGGICCAAGGAGCTCGCTCGAGGCGCC	
ONAPTADA.....GG.....T.....	2371
DNAPTTRC.....C.....T.....C.....C.....	2371
DNAPTTHC.....C.....C.....C.....C.....	2380
MAJORITY	CCAAACACCGCGCCGAGCGTGGCCGCTTTCGCCAAGGAGGCTCATCGAGGCGCTCTATCGCCCTCGCCCT	
ONAPTADA.....CC.....CGGC.....C.....	2444
DNAPTTRC.....C.....AG.....A.....C.....C.....C.....C.....	2441
DNAPTTHC.....C.....C.....A.....C.....AA.....C.....C.....	2450

FIGURE 3

MAJORITY (SEQ ID NO:8)	HXAWLP L FEPKGRVLLVOGHHLAYRTFFALXOLTISRCEPVOAVYGFAKSLLKALKEEC DAVXVVFOAK	
TAQ PRO (SEQ ID NO:4)	AG.....H.....I..... 139
TR PRO (SEQ ID NO:5)V.V..... 138
TTM PRO (SEQ ID NO:6)	E.....YK.F..... 140
MAJORITY	APSFARAEAYKACRAPTPEOPROLALIKELVOLLGLXALEVPGYEADOVLAFLAKXAEKECYEVAIL	
TAQ PRO	GG.....	A.....S.....
TR PRO	U.....F.....A.....
TTM PRO	F.....
MAJORITY	TADRDLYOLLSDRIAVLHPEGYLIIPAWLWEKYGLRPEQWVDYRALXODPSDHLPGVKGICENTAXKLLX	
TAQ PRO	K.....H.....	D.A.....Y.....E.....A.....E 209
TR PRO	E.....I.....	Y.....A.....I.....OR.IR 208
TTM PRO	V.....V.....H.....E.....	F.V.....L.....K 210
MAJORITY	EWGSLLENLKNLORVKP.XXREKIXAHMEDLXLSXXLSXVATOLPLEVDFAXAREPDREGLEAFLEALCF	
TAQ PRO	A.....L...AI...L...D...K...WD.AK.....	K.....A..... 278
TR PRO	FOH.O...SL...LQ.G...A.A.AX.O.H.....	GR.I.NL..... 277
TTM PRO	ENV...K...L...A...LE.A.....	L.QC..... 280
MAJORITY	GSLLEFGLLXPKALCEAPWPPPEGAFVGFVLSAPEPMWAEELLALAAARXCARVHRAAXOPLXGLROLKXEV	
TAQ PRO	S.....	K.....D.....C.....PE.YKA.....A 348
TR PRO	G...A...L...SF.....	C.WE...L...Q...R...G... 347
TTM PRO	A.AP.....	K...C.D...A...A...K..... 350

//

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	ACLLAKOLAVLALREGLQIXPGDDPHLLAYLLOPSHTTPEGVARRYGCEWTFEDAGERALLSERLFXNLXX	
1AD PRO (SEQ ID NO:4)	S.....G.P.....	A.....A.....A.....WG
TR PRO (SEQ ID NO:5)	I.....F.E.....	A.....A.....QI.KE
TH PRO (SEQ ID NO:6)	S.....V.....	AH.....HA...LK 420
MAJORITY	RIEGEERLLWLYXEVEKPLSRVLAHMEATGVRLDVAYLQALSLEVAEEIRRLSEEEV78LACHPFFHLSRAO	
1AD PRO	R...R...A.....	R.....A.....A.....488
TR PRO	E.....A.....	EA.V.O.....487
TH PRO	K.....H.....	L.....490
MAJORITY	OLEARVLFDELGLPAIGKTEKTKXASTSAUVEALREAHPIVEKILQYRELTKLKNTYIDPLXLVHPRTG	
1AD PRO	S.....D.I.....558
TR PRODR.....	A.....K...557
TH PRO	A...L...Q.....	H.....V...S.....560
MAJORITY	RLHTRFNOJATATGRLSSSDPHLQHPVATPLGQRI RRAFVAEEGWXLVALDYSOIELAVLAHLSCDNL	
1AD PRO	L.....628
TR PROV...V.....	627
TH PROA...A.....	630
MAJORITY	I AVFOEGRODHTQTASWMF GUPPEAVDPLMRRAAKTINFGVLVGMSAHRLSOELAI PYEEAVAFIERFFO	
1AD PRO	E.....R.....	O.....698
TR PRO	S...G.....	G...S.....697
TH PRO	K.....V.....700

FIGURE 3 (cont'd)

MAJORITY (SEQ ID NO:8)	SFPKVRWIEKTL EECRRRCYVETL FORRRYVPDLNAAVKSVREAAERMAFNMPVQOTAADLHKLAMVXL	
IAQ PR0 (SEQ ID NO:4)	769
TEL PR0 (SEQ ID NO:5)	Y.....	767
TTM PR0 (SEQ ID NO:6)K.....	770
MAJORITY	FPRLEXMGARMLOVHDELVL EAPKXRAEXVAAALAKENVHEGVYPLAVPLEVEVGXGEDWLSAKEX	
IAQ PR0E.....	833
TEL PR0O.L.....	831
TTM PR0R.....	835

FIGURE 5

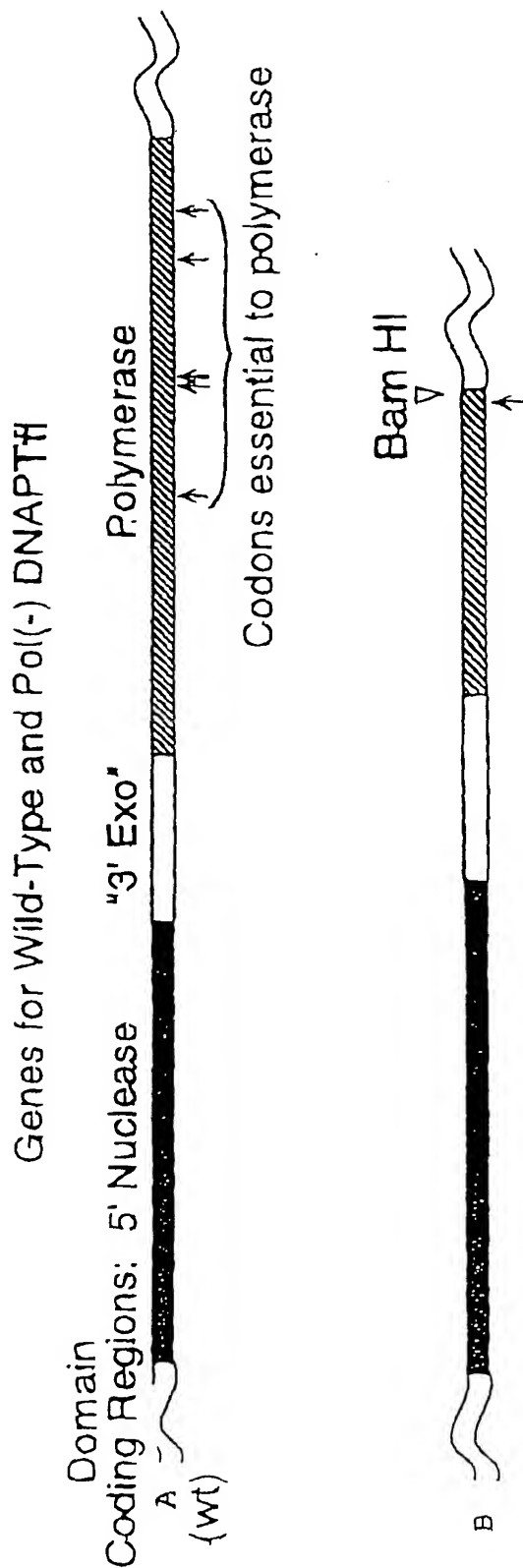


FIGURE 6

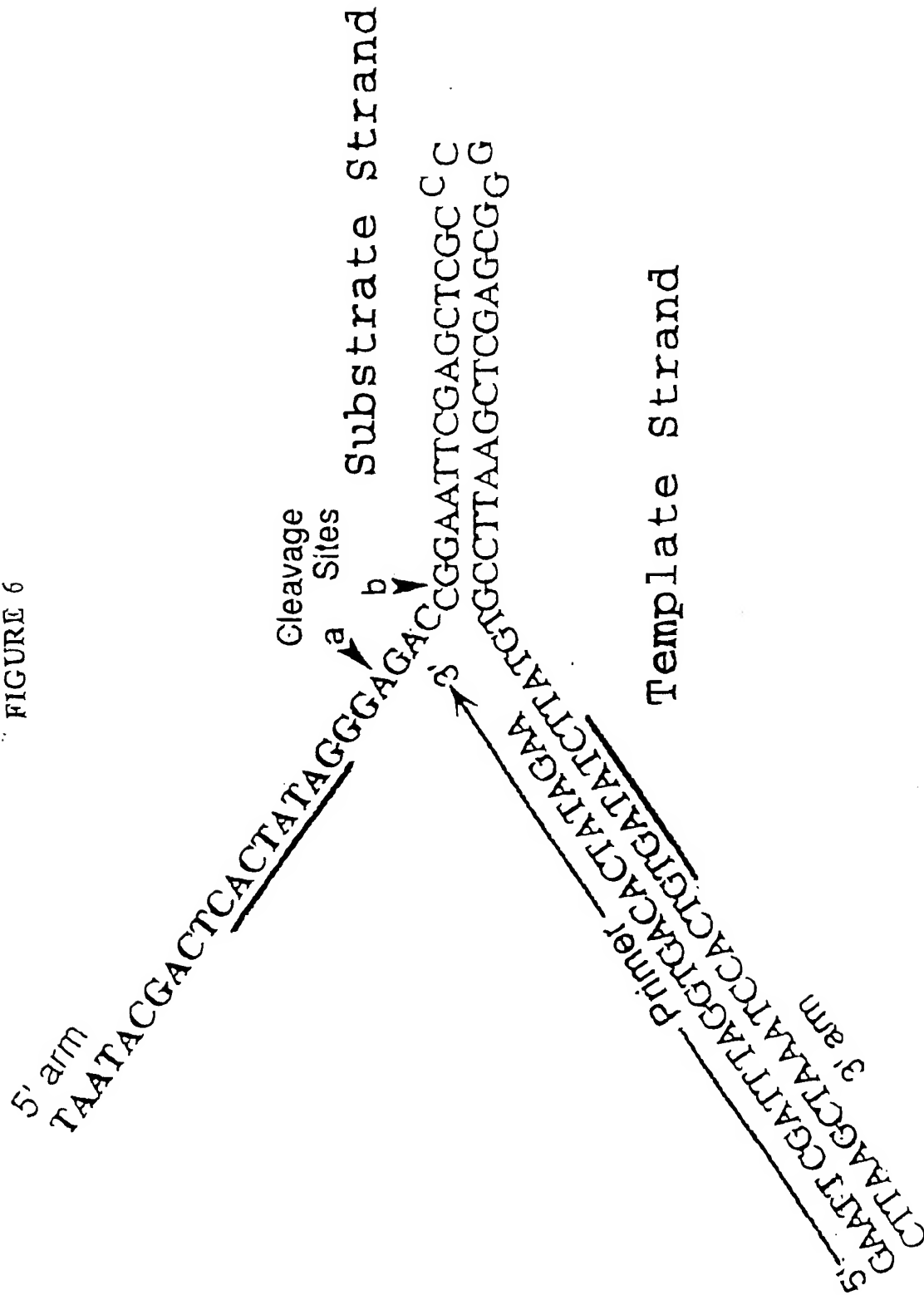


FIGURE 7

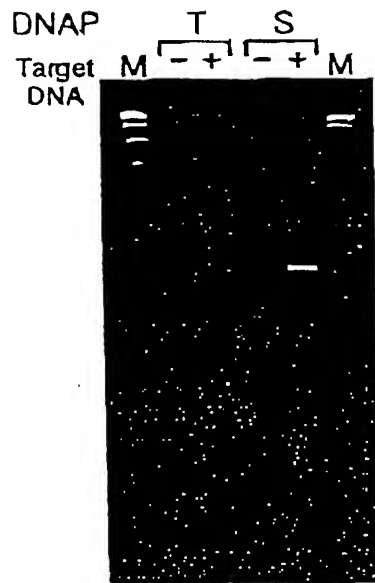


FIGURE 8

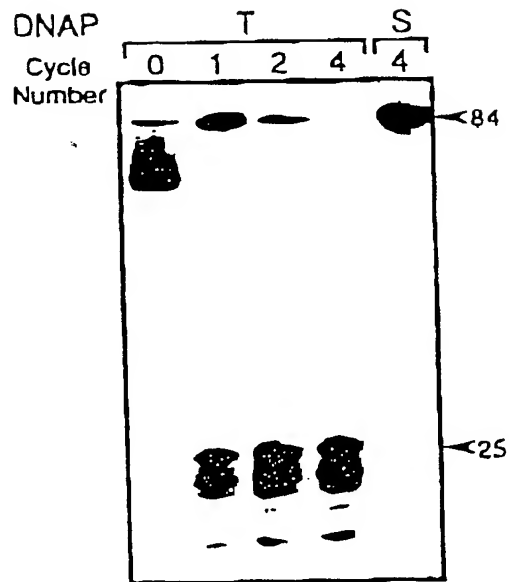


FIGURE 9

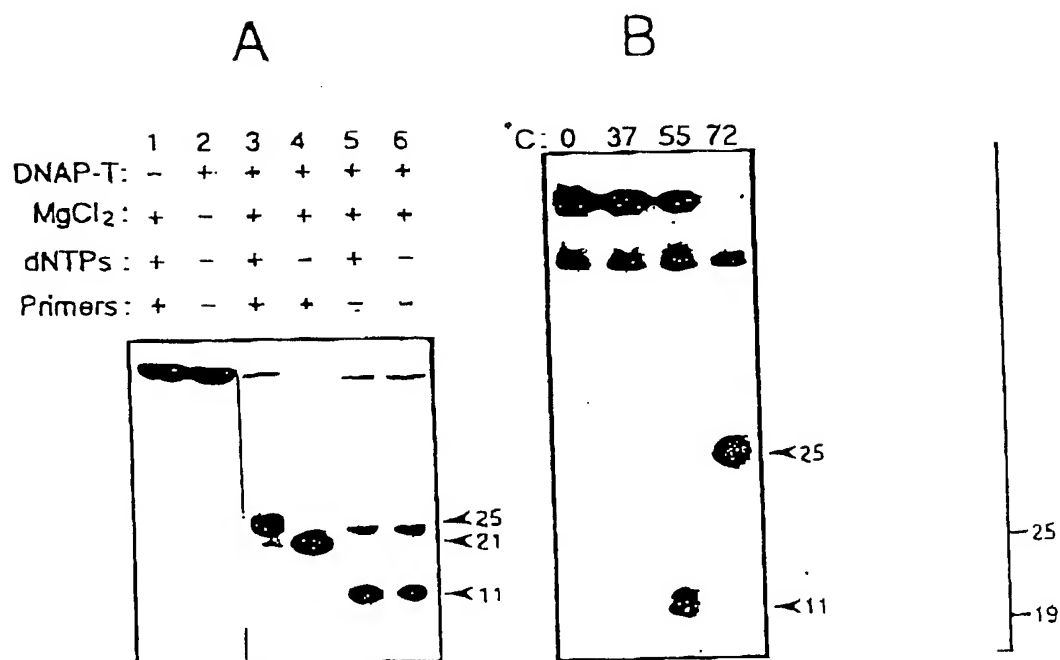


FIGURE 10

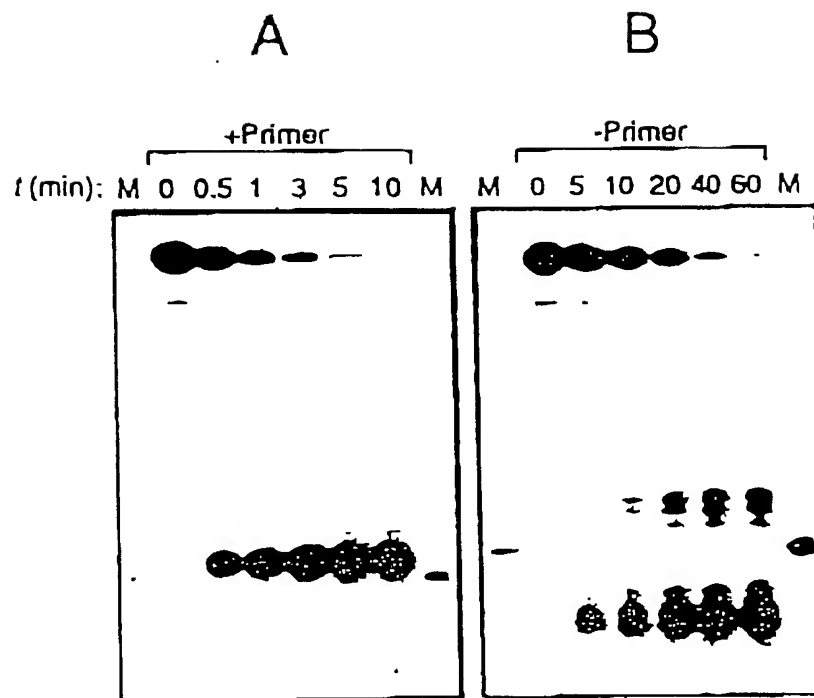


FIGURE 11

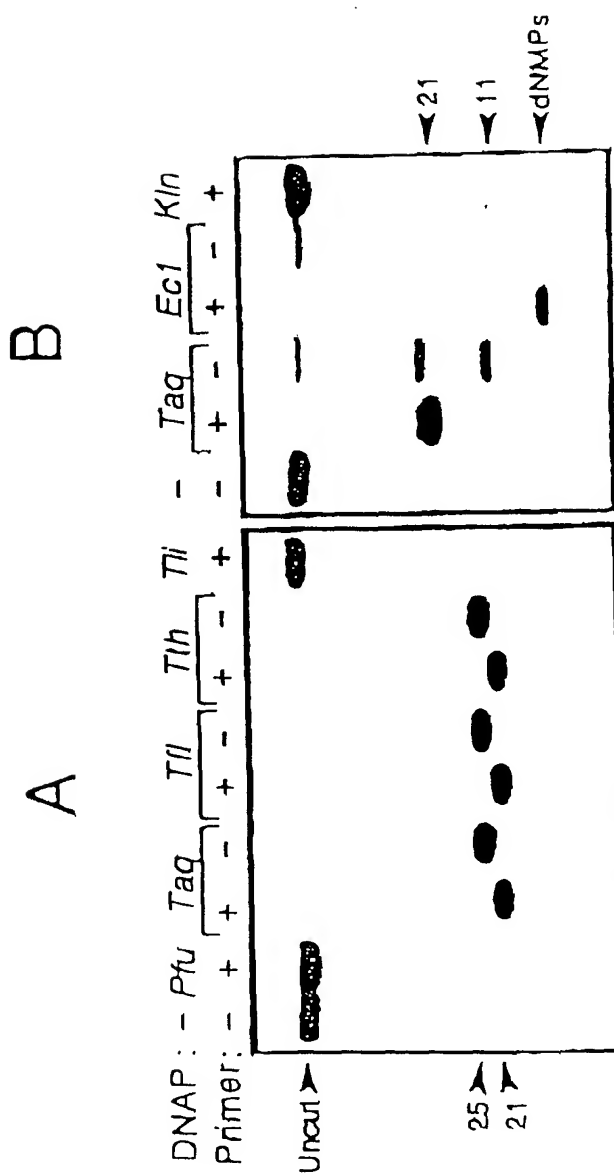


FIGURE 12

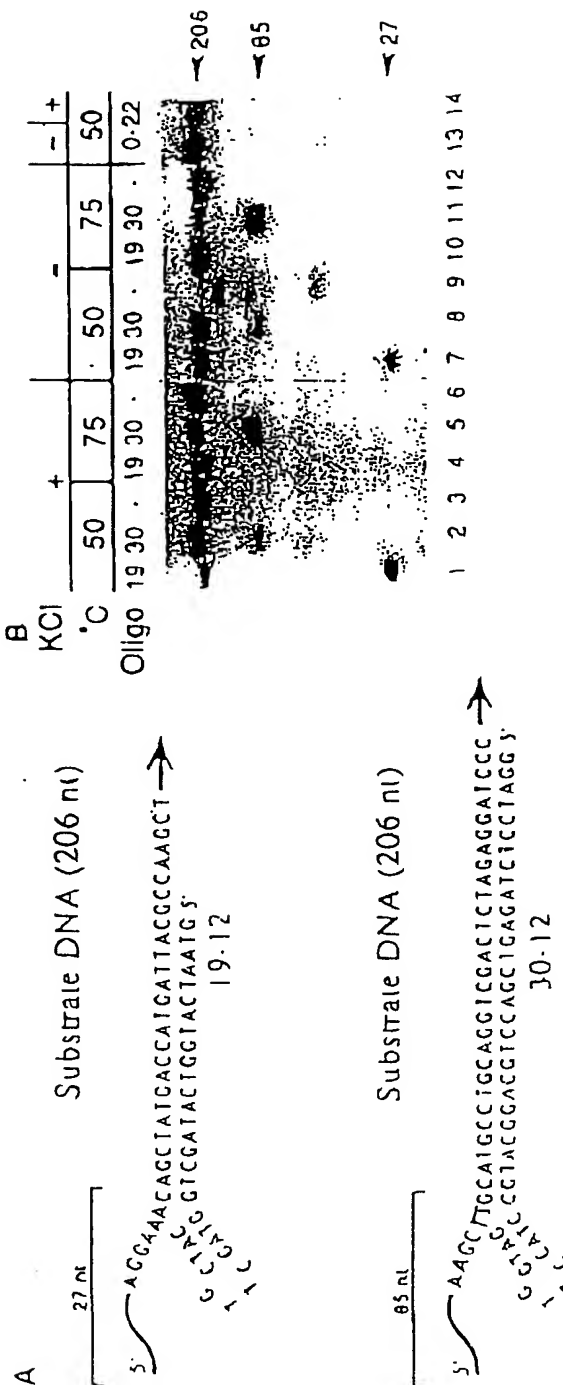


FIGURE 13

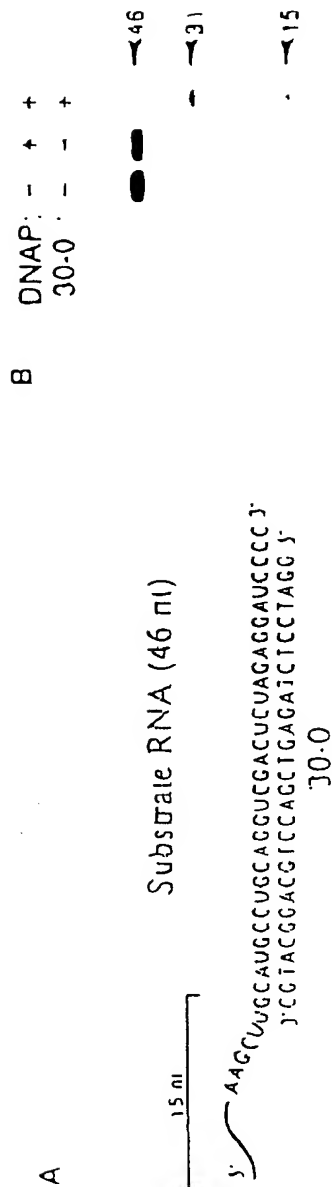


FIGURE 14

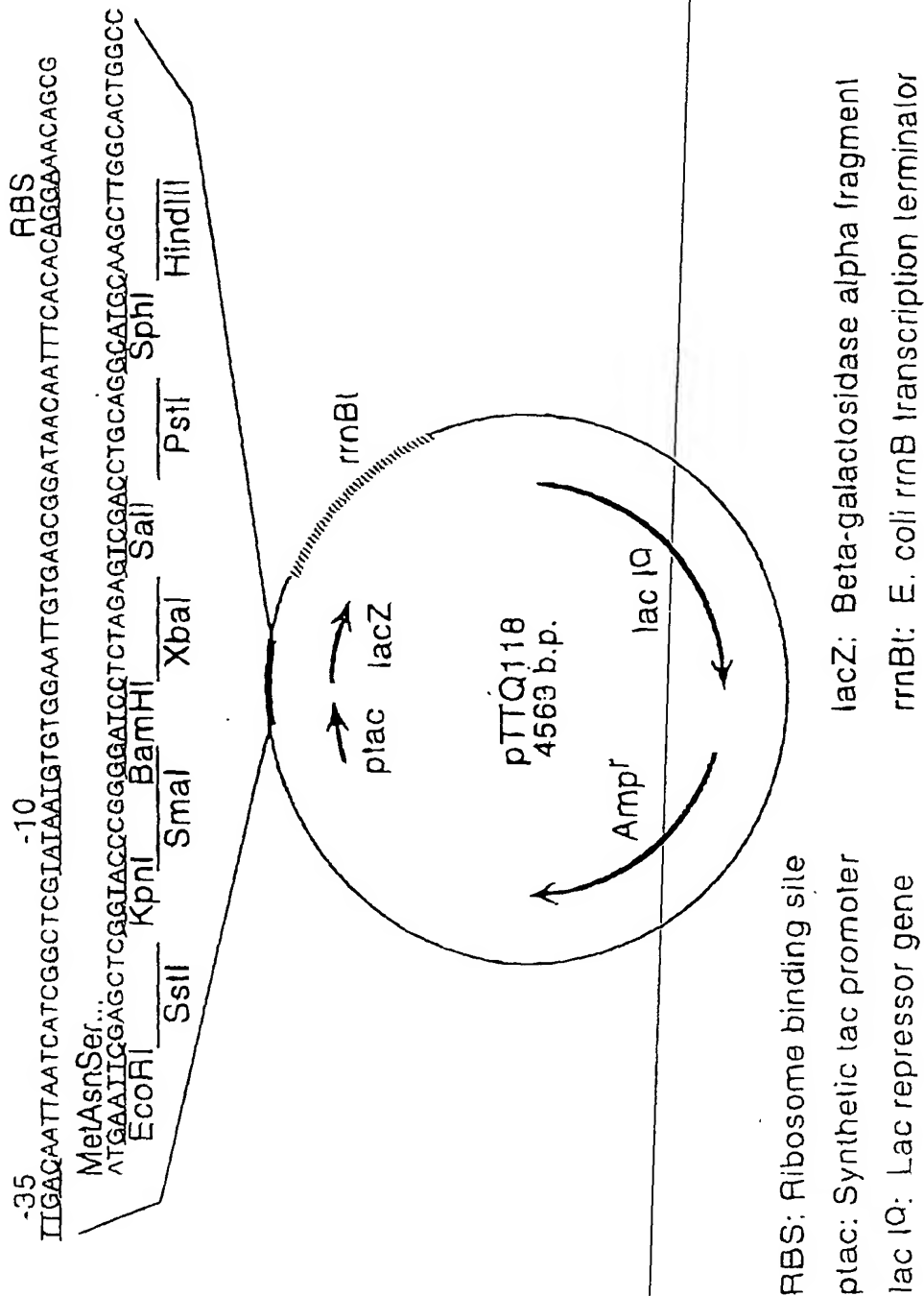
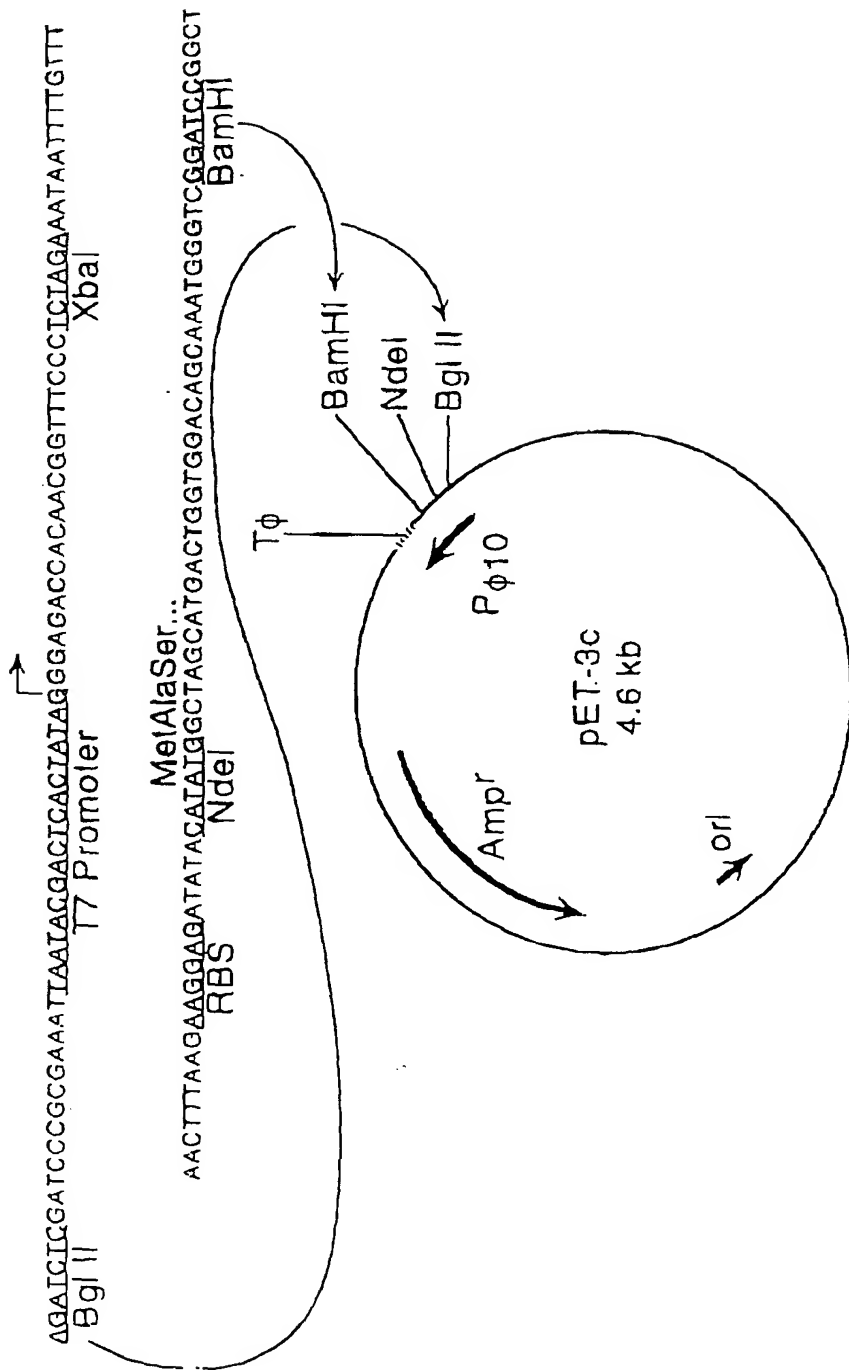


FIGURE 15



P ϕ 10: Bacteriophage T7 ϕ 10 promoter
T ϕ : T7 ϕ Terminator
RBS: Ribosome binding site

FIGURE 16

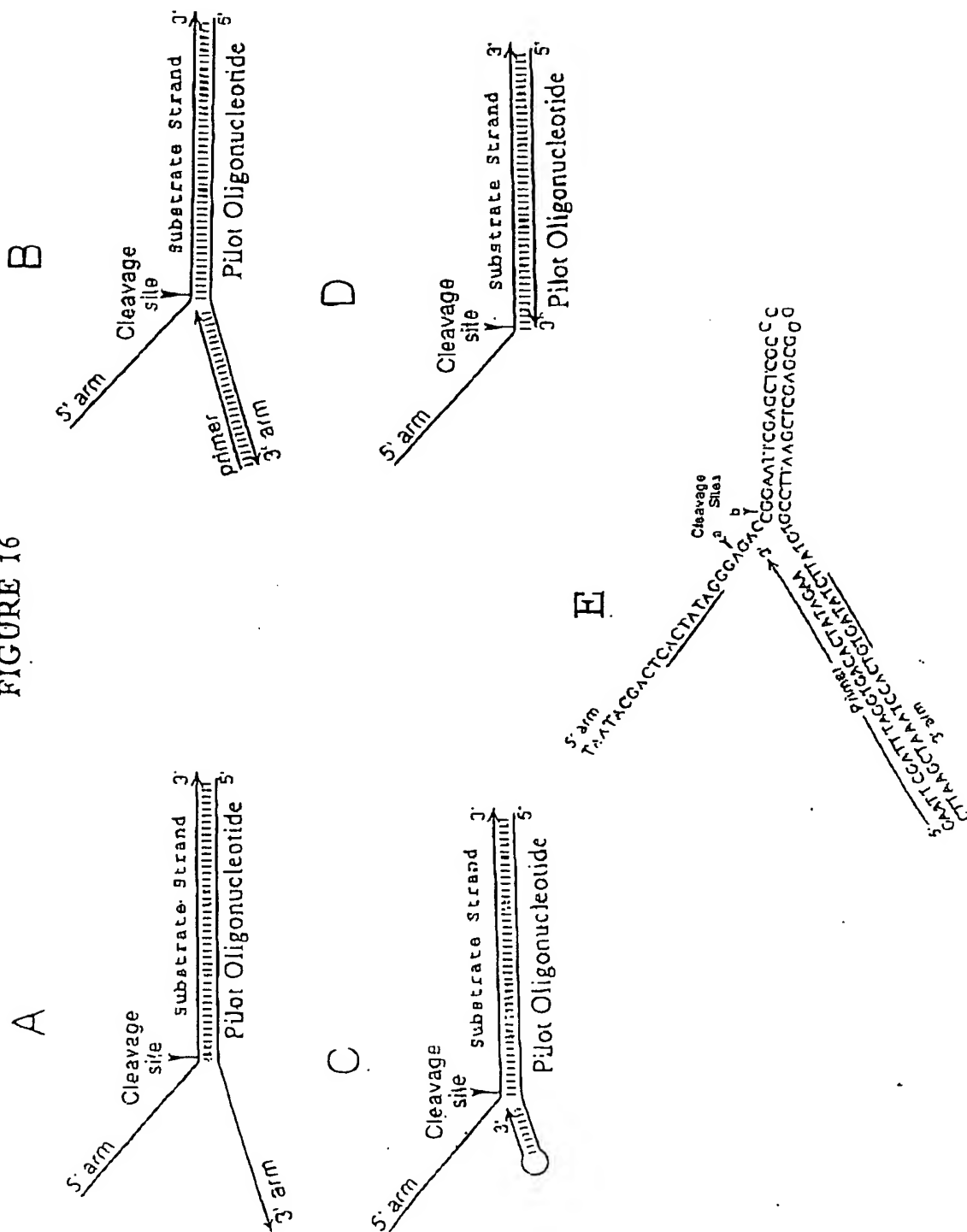


FIGURE 17

1 2 3 4 5 6 7

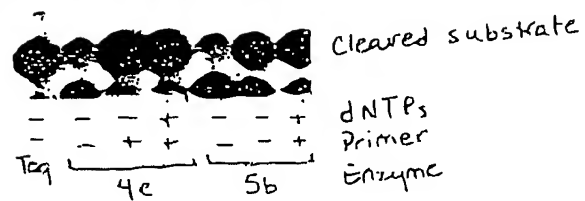
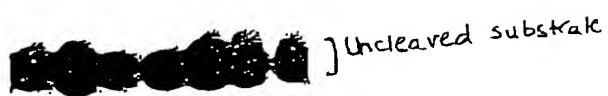


FIGURE 18

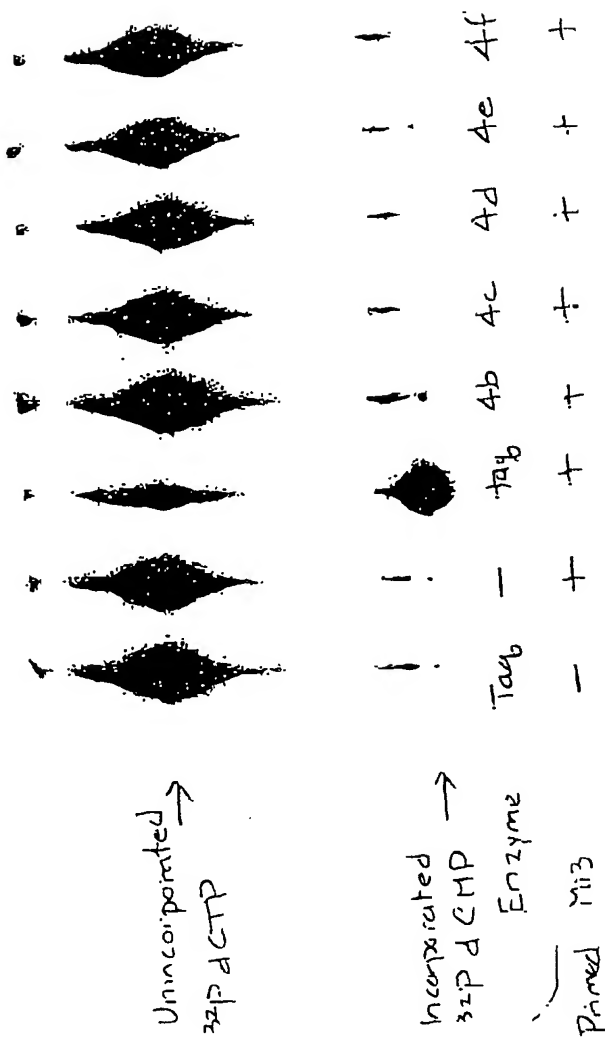
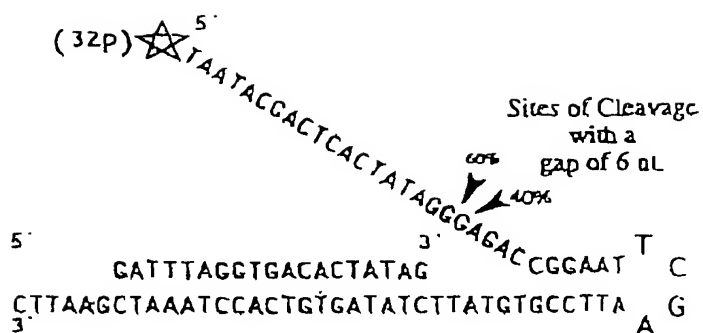


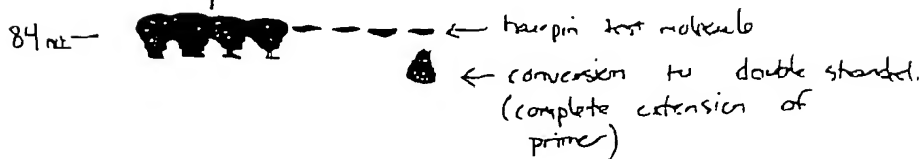
FIGURE 19

A

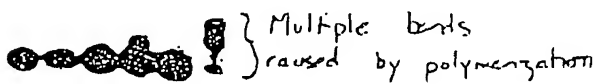


B

4d				4b		Unmodified	
No				(2 pr. mutation)		DNAT Tag	
Rel. Activity				small activity			
1	2	3	4	5	6	7	8
C/A				T/A		T/A	
+				-		+	



desired product
21 nuc.



some aberrant cleavage with 4b because of residual polymerase activity.

Diagram illustrating a DNA hairpin structure, showing two regions: A-Hairpin and T-Hairpin.

A-Hairpin:

Sequence: 5' --CGGACGAAACAAGCGACACACCGACACAGI A

Complementary sequence: GTACC C, CATGG A

T-Hairpin:

Sequence: 5' GTTTCGCGGTCTCTCTCTCTTTI A

Complementary sequence: CTACC T, CATGG C

Arrows indicate predicted cleavage sites at the ends of the hairpin stems.

C

5' ACACAGT A

GTACC C

CATGC A

T

"Tau" →

5' CAAACACgACACAgCAGAgAgAACCCACAA

Cleaved A-Hairpin

5' CTTCTTT A

CTACC T

CATGC C

T

"Alpha" →

5' -CTGCTGTTCGCTCTGTGCGCTGTGTC-

3'

Cleaved T-Hairpin

D

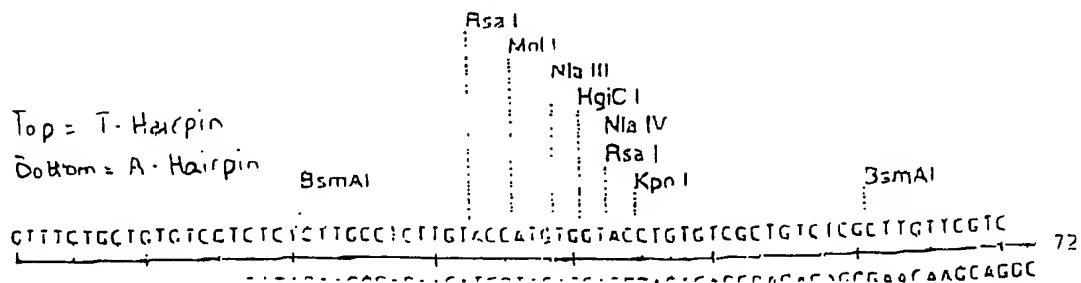


FIGURE 22A

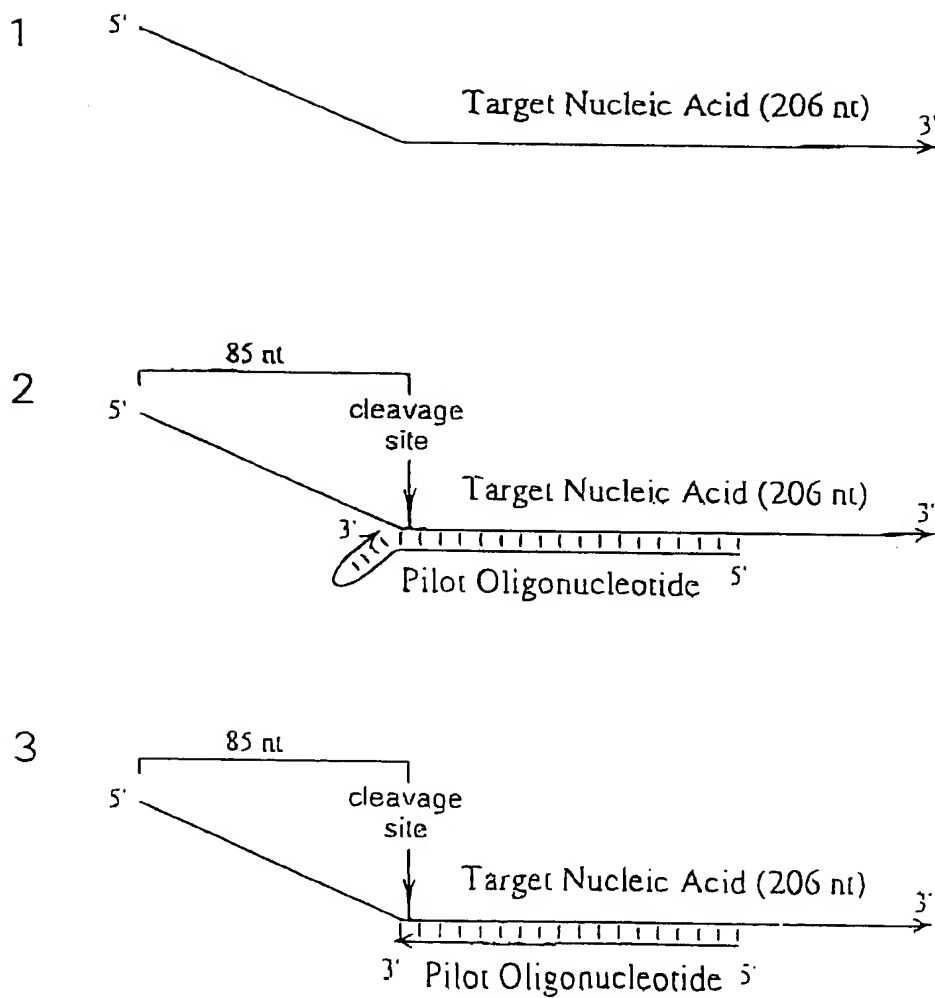


FIGURE 22B

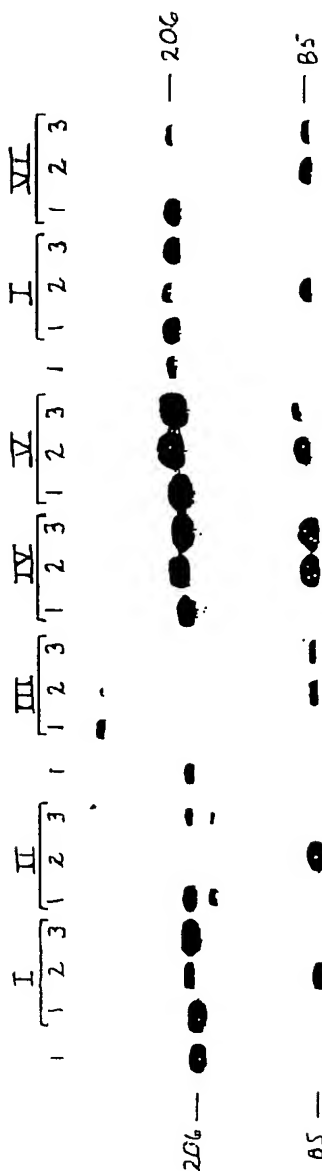


FIGURE 23

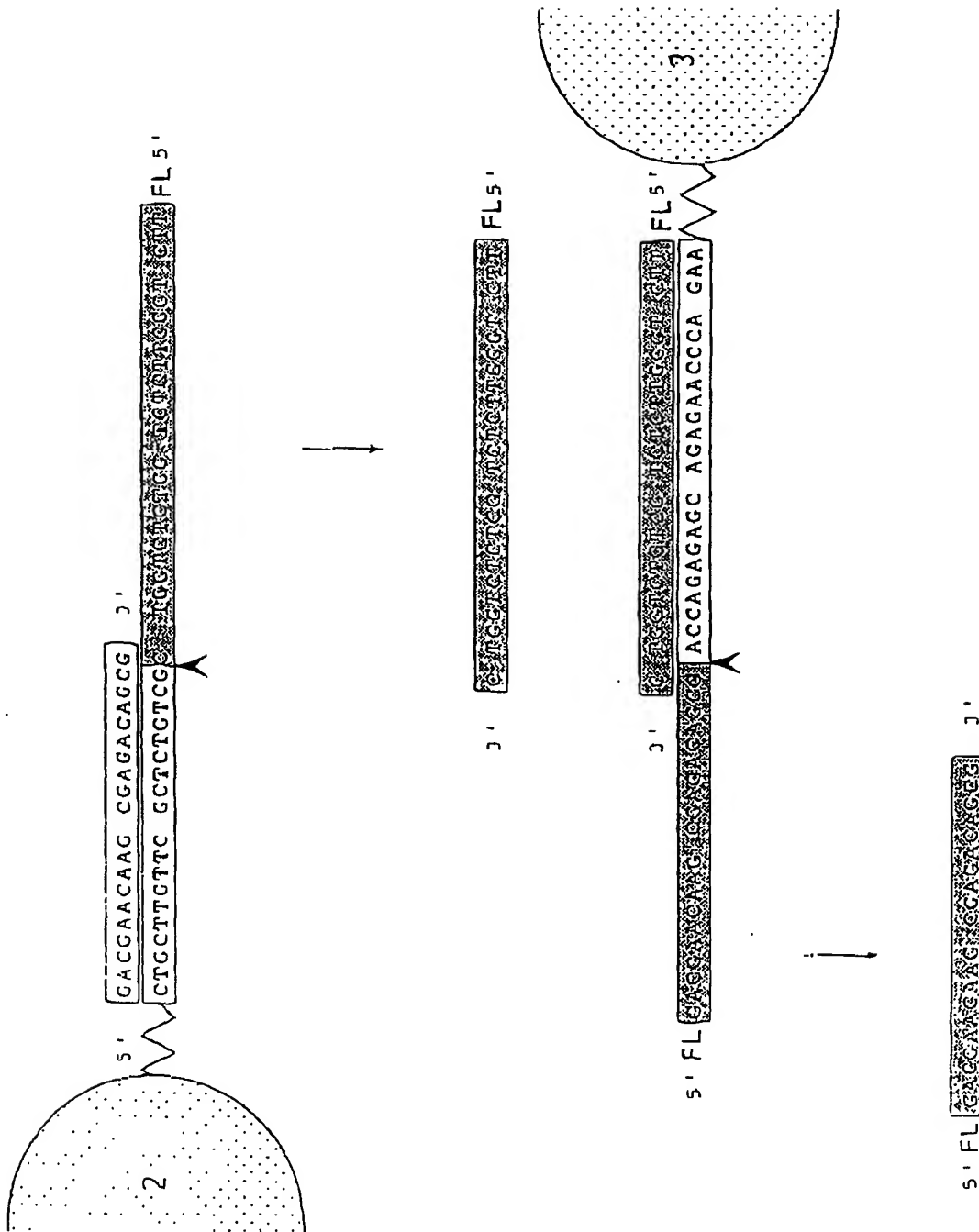


FIGURE 25

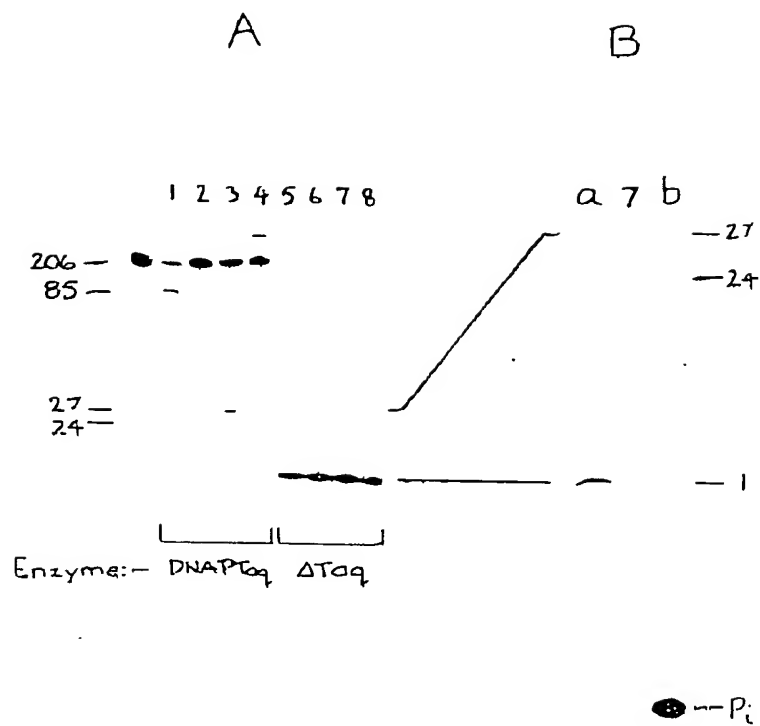
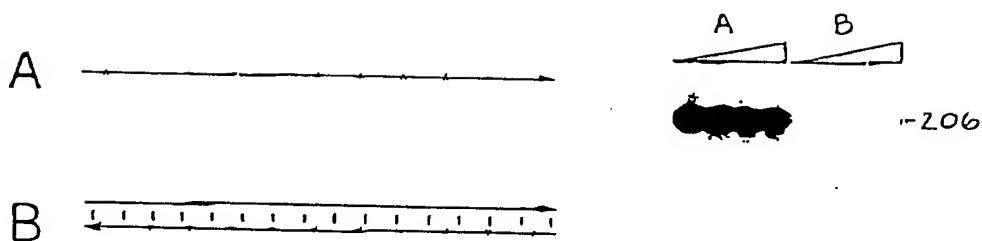


FIGURE 26



$\approx 32\rho$

FIGURE 27

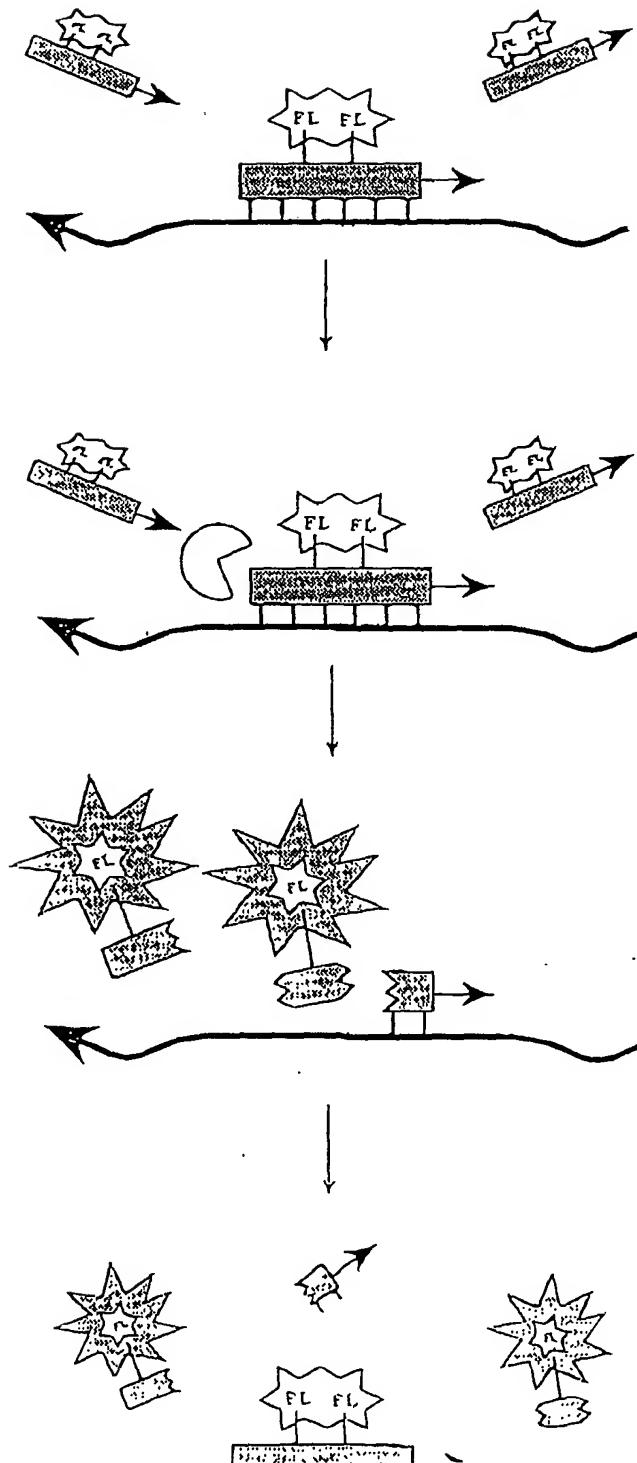
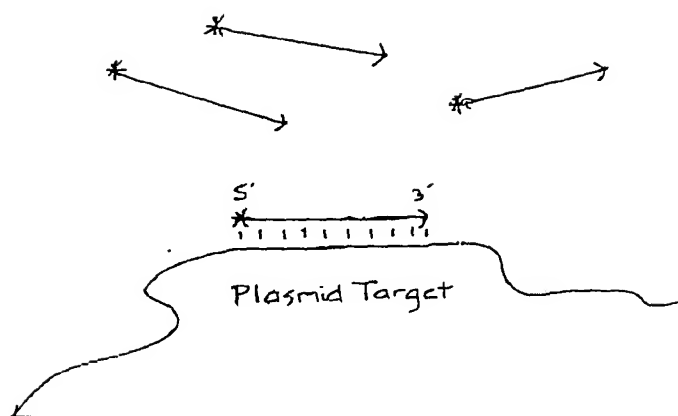


FIGURE 28A



* = ^{32}P S' terminal phosphate

FIGURE 28B

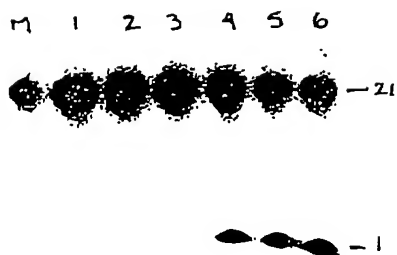


FIGURE 29

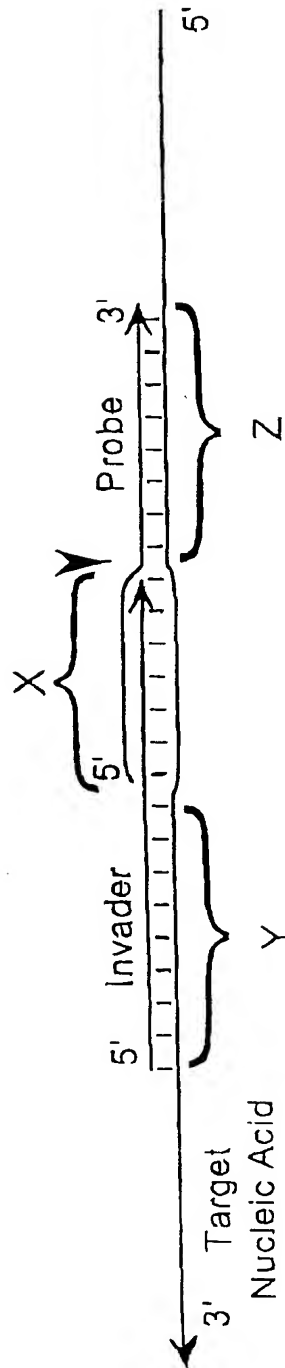


FIGURE 30

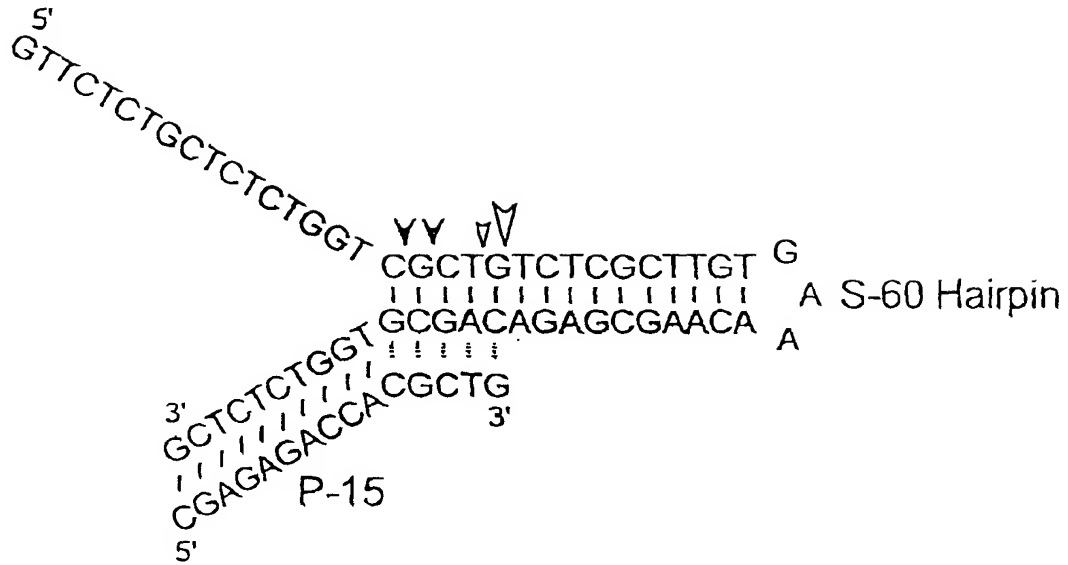


FIGURE 31

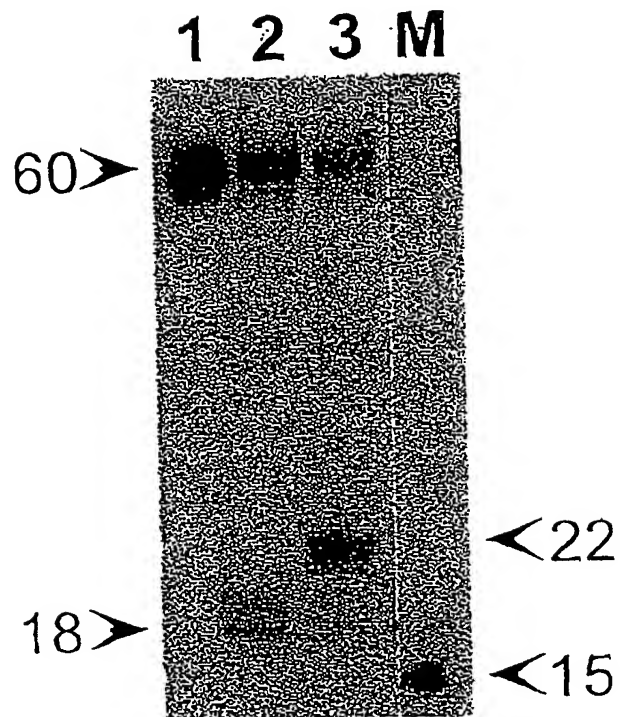
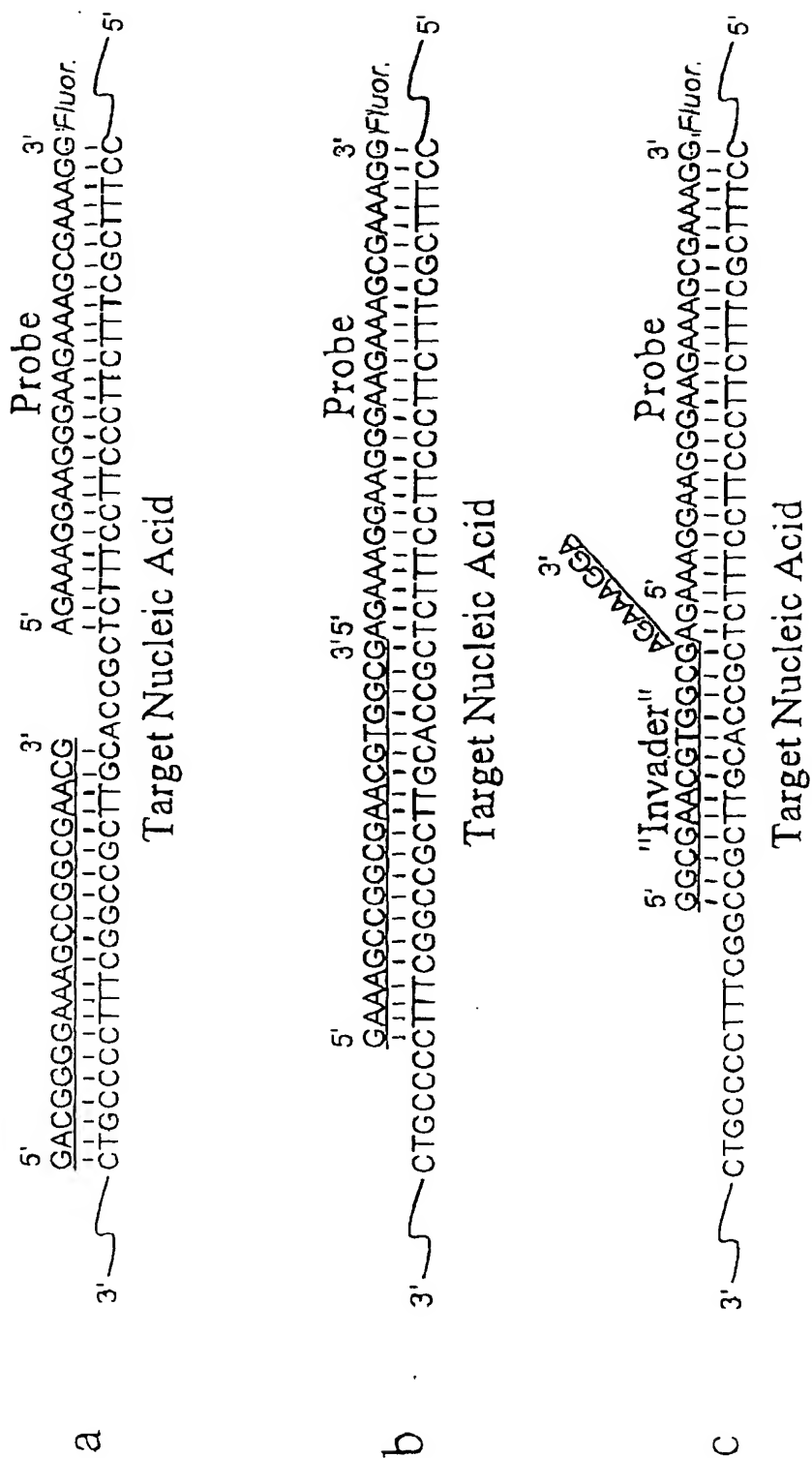


FIGURE 32



8

7

6

5

4

3

2

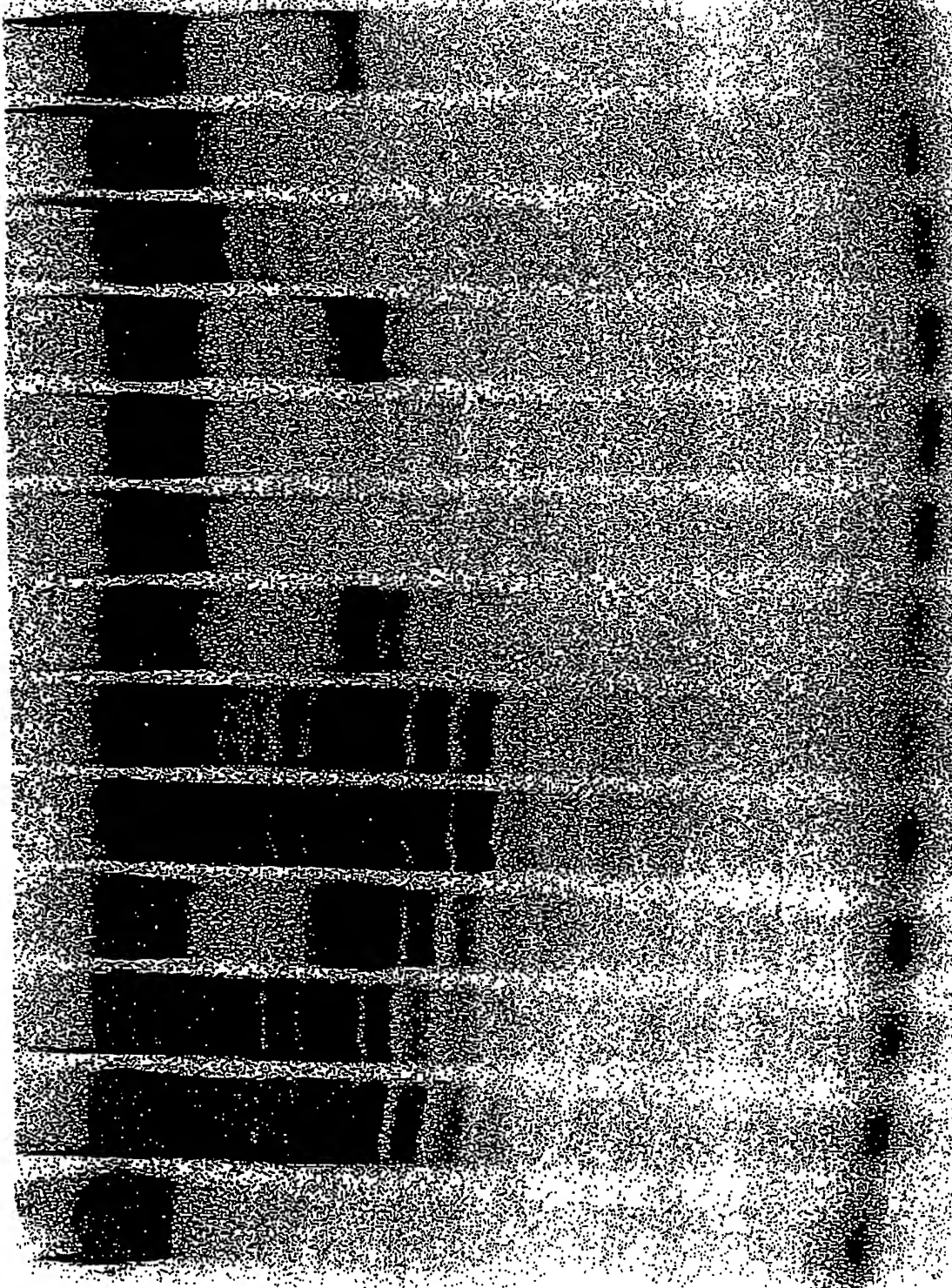
1

6

45

FIGURE 34

M 1 2 3 4 5 6 7 8 9 10 11 12



A

46

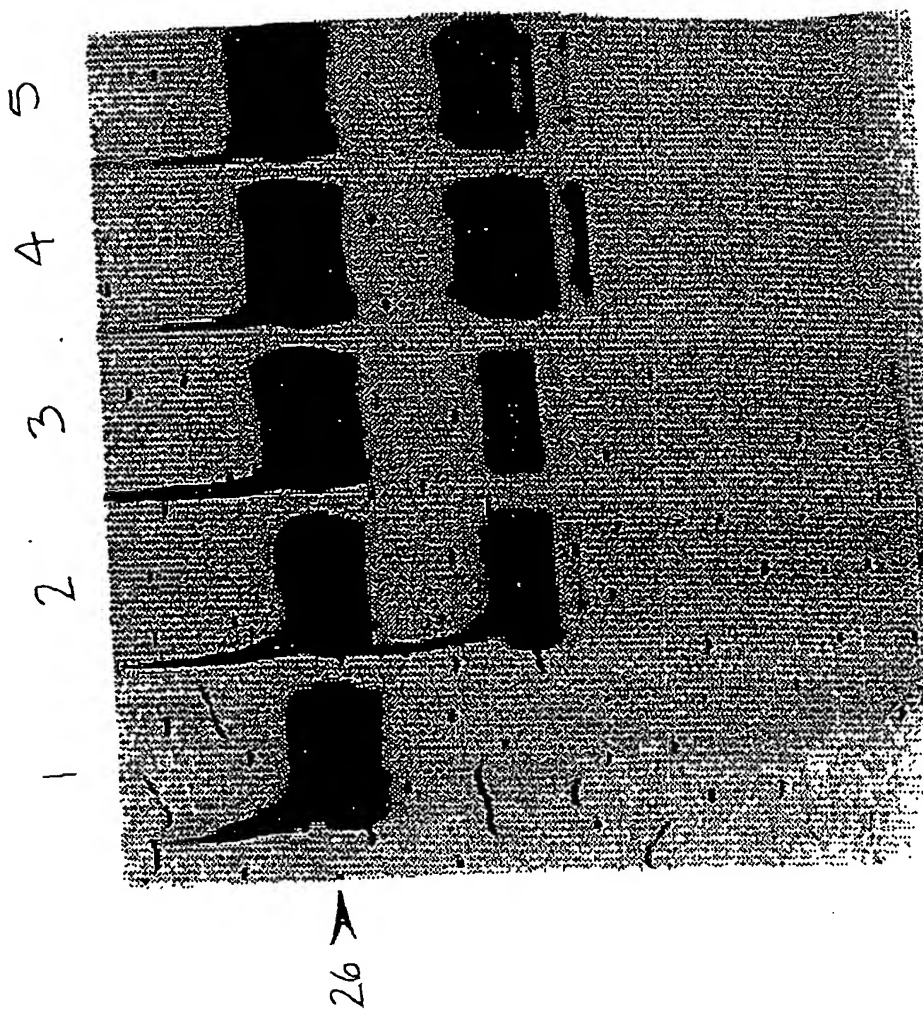
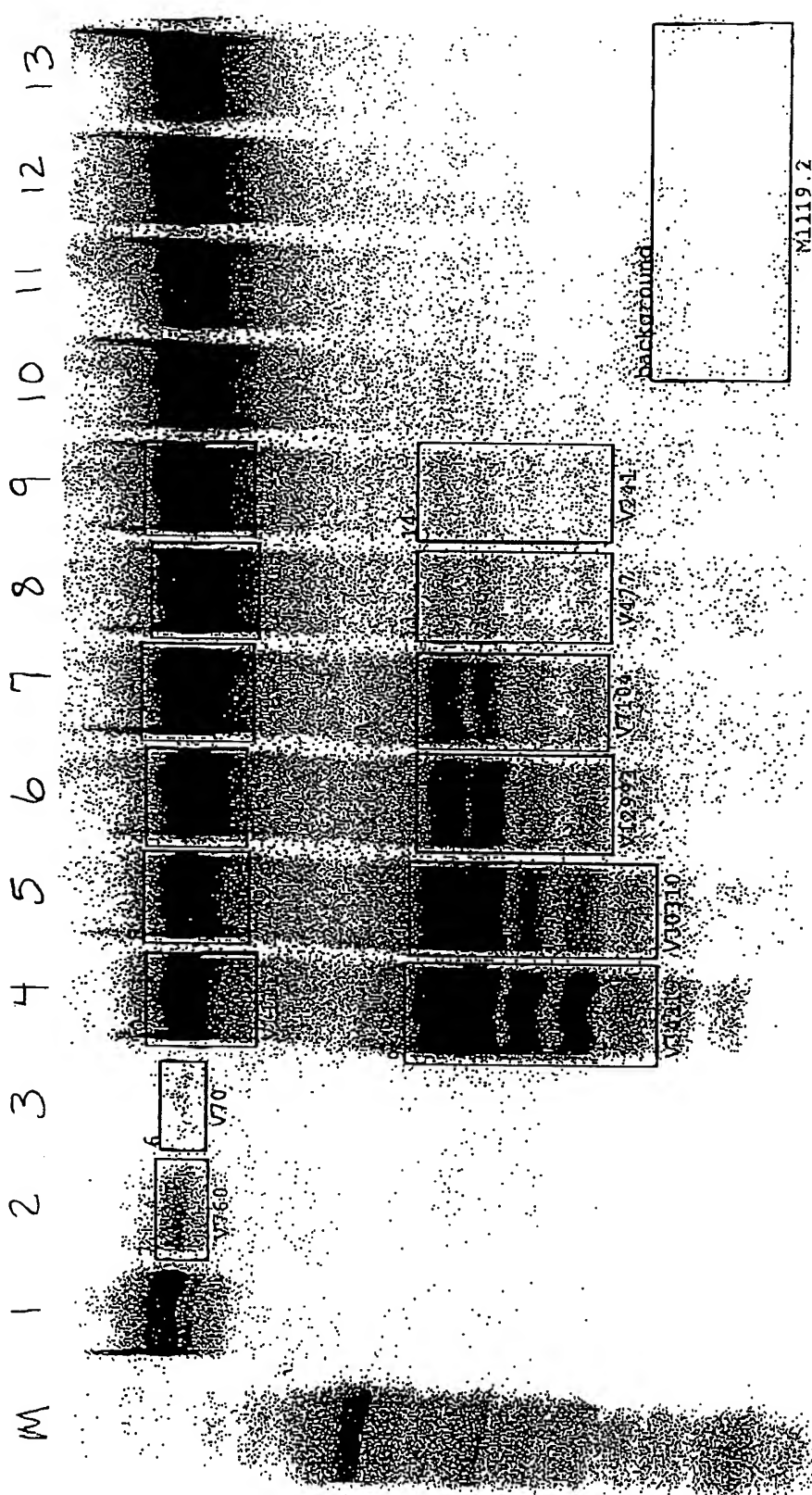
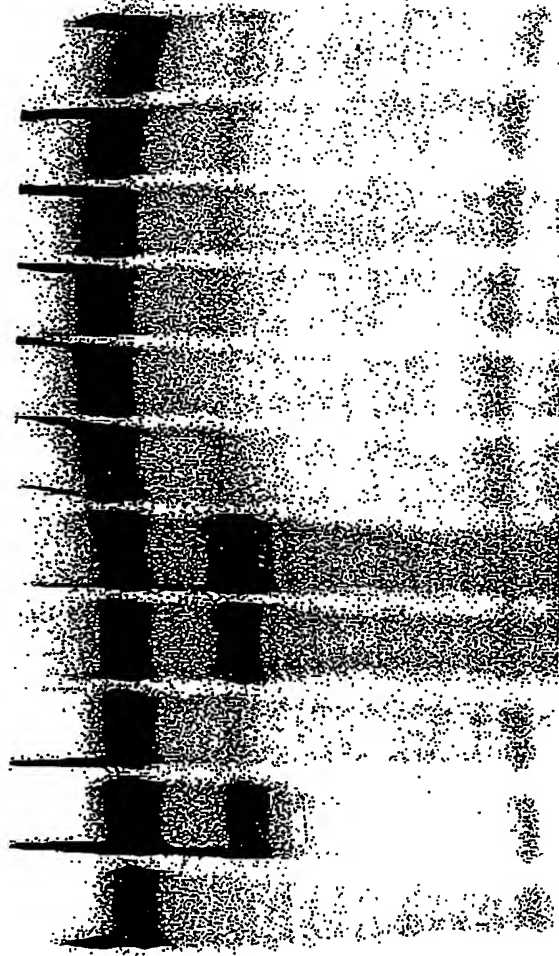


FIGURE 36



1 2 3 4 5 6 7 8 9 10 11



A

A

FIGURE 38

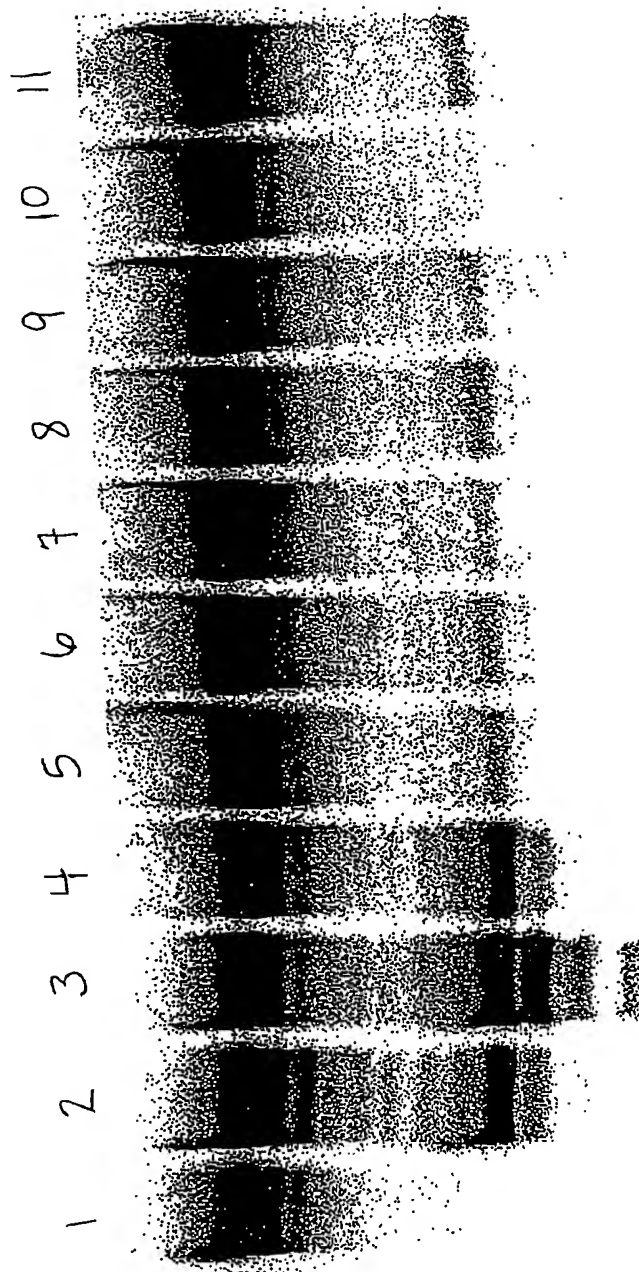


FIGURE 39

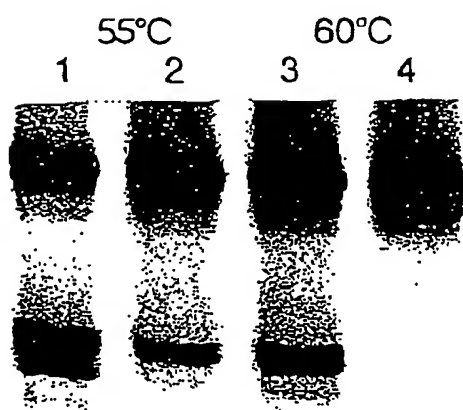


FIGURE 40

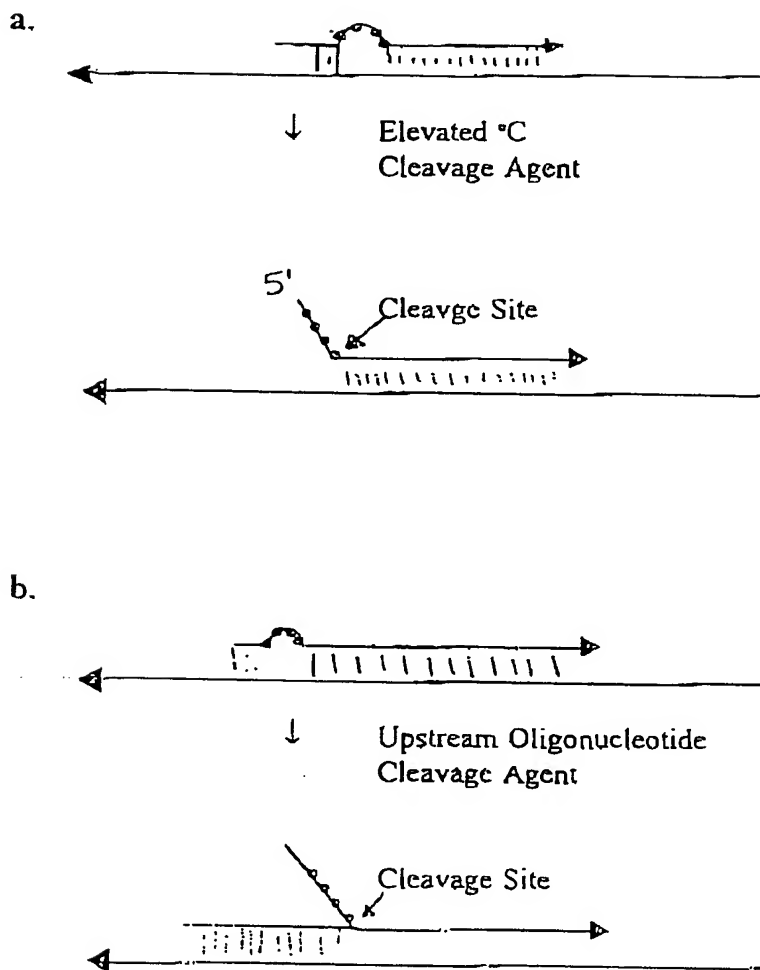


FIGURE 41

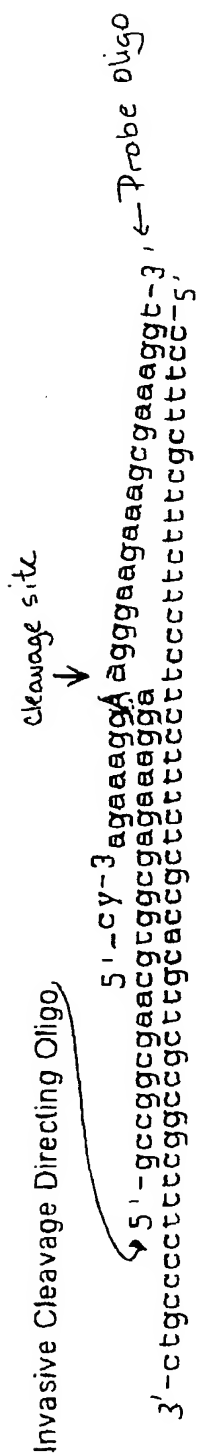


FIGURE 42

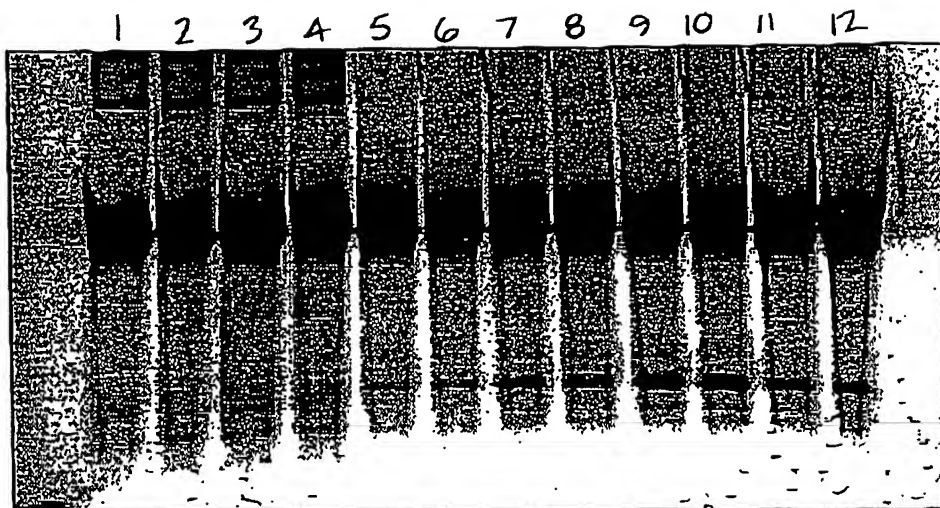


FIGURE 43

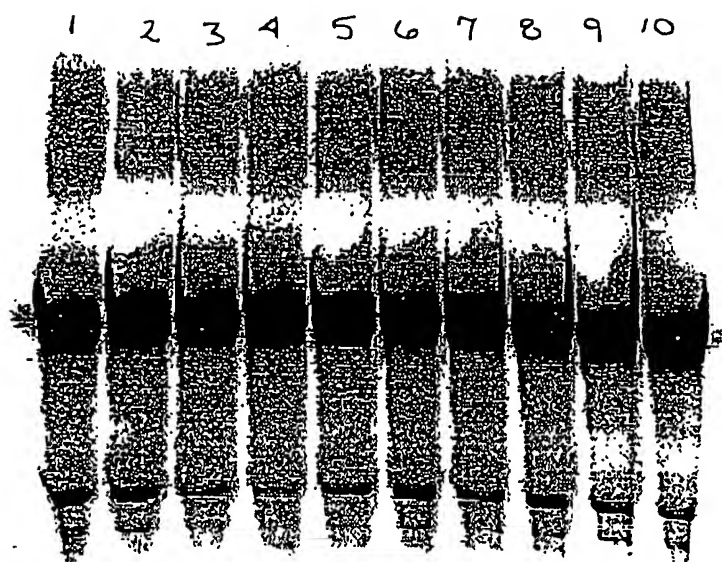


FIGURE 44

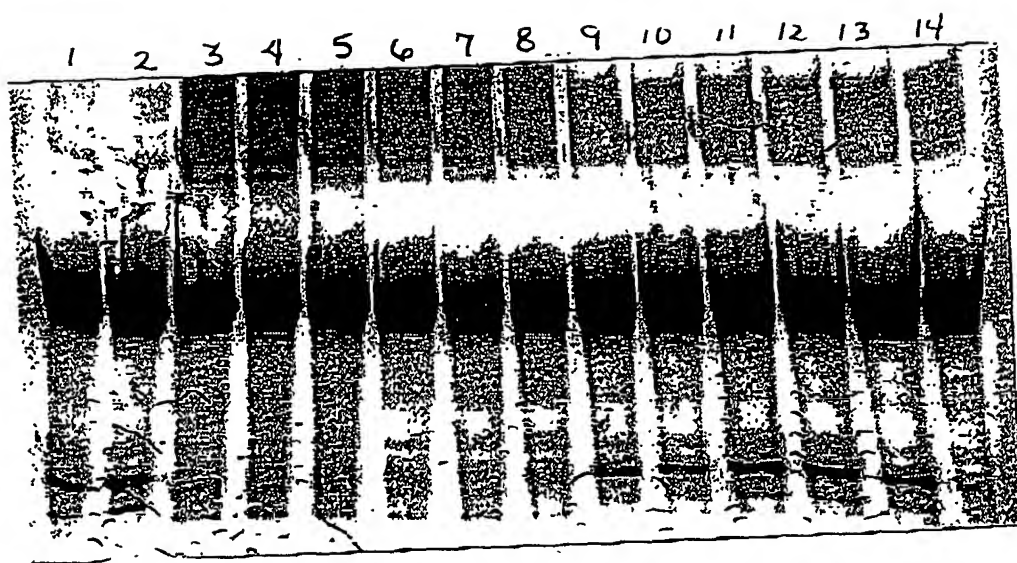


FIGURE 45

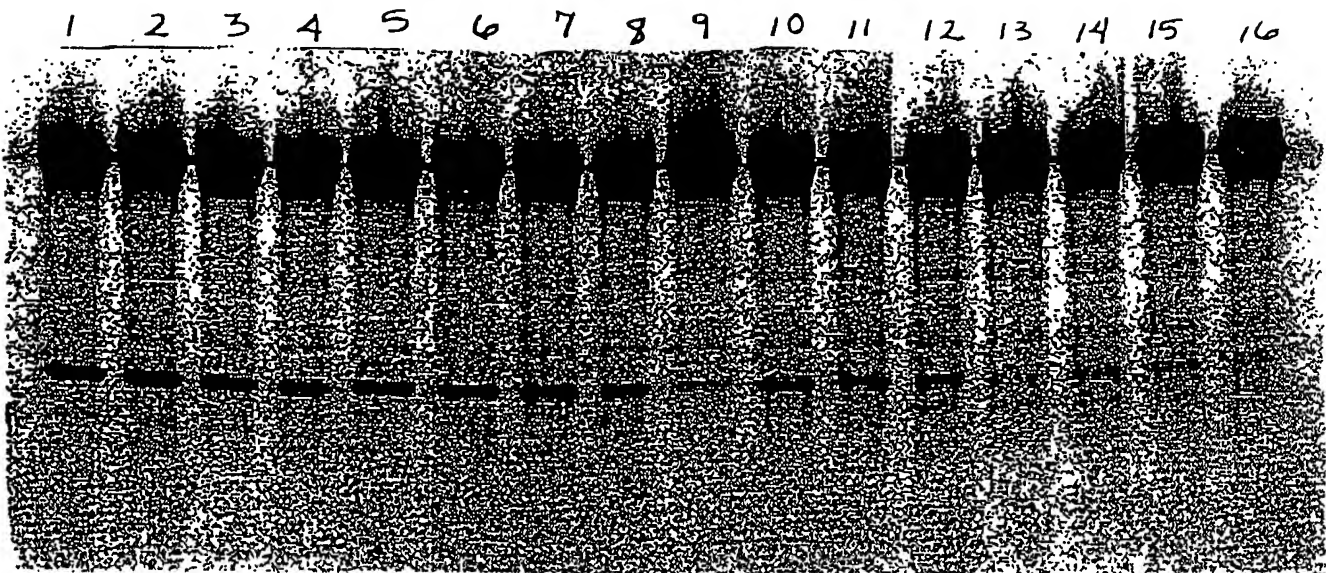


FIGURE 46

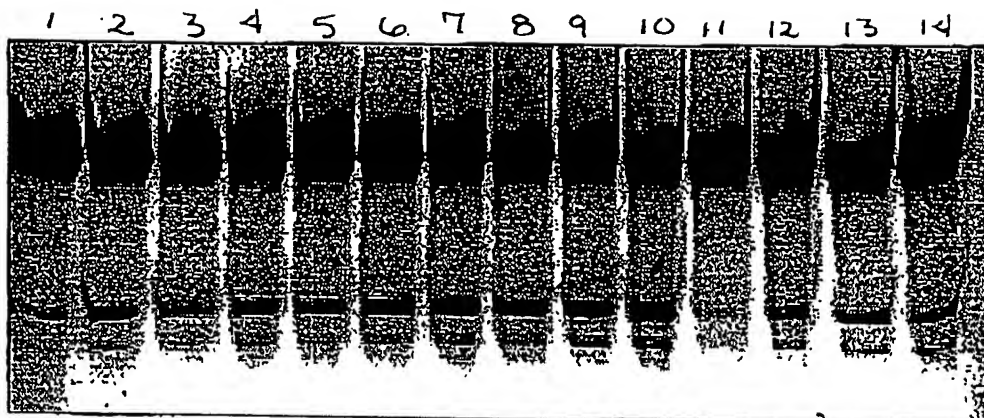


FIGURE 47

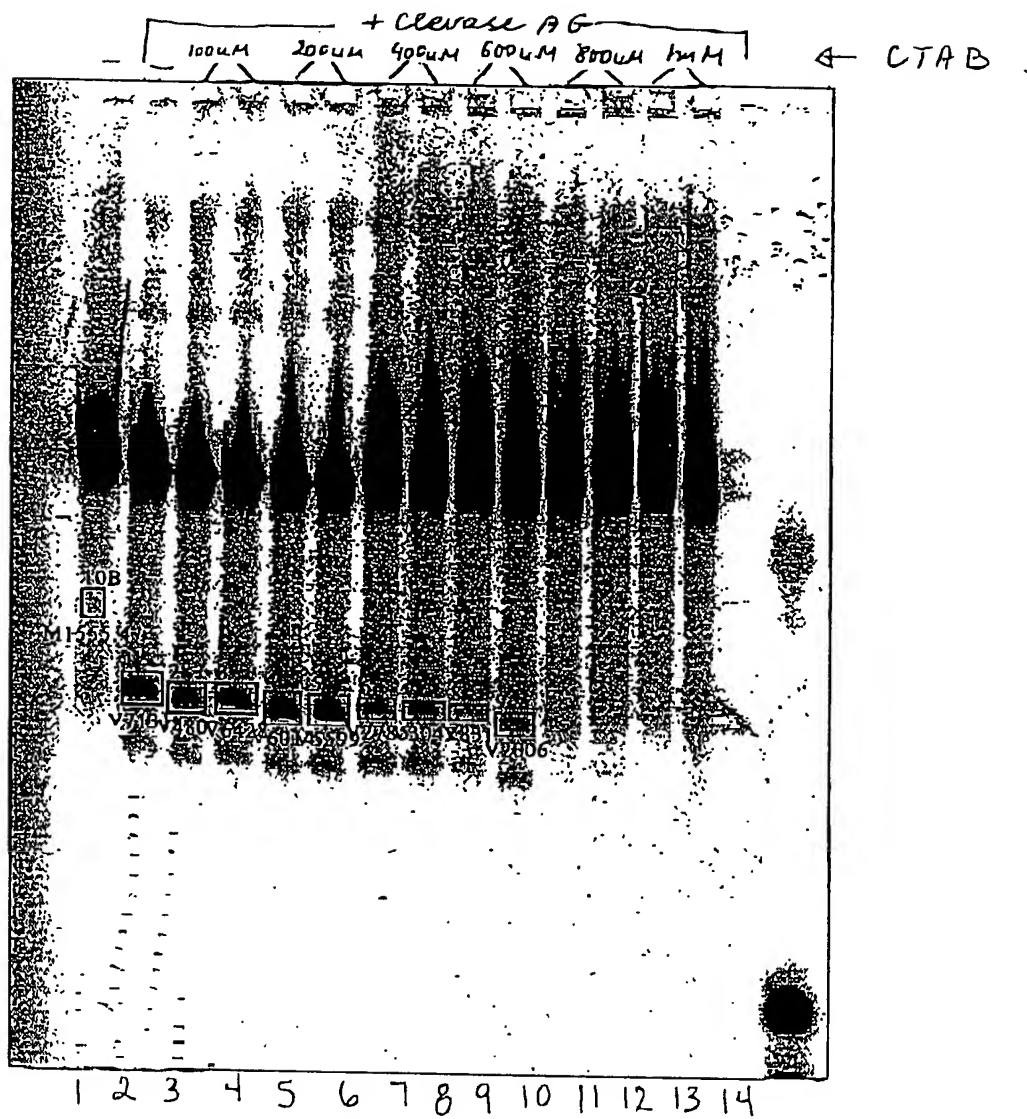


FIGURE 48

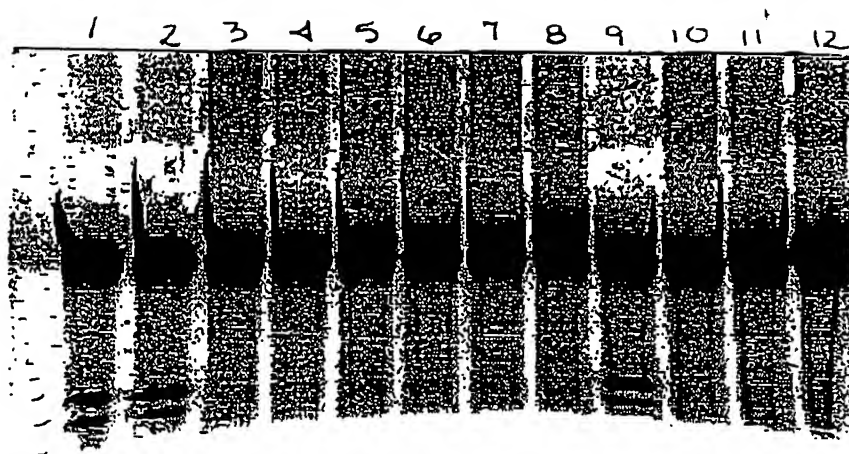


FIGURE 49

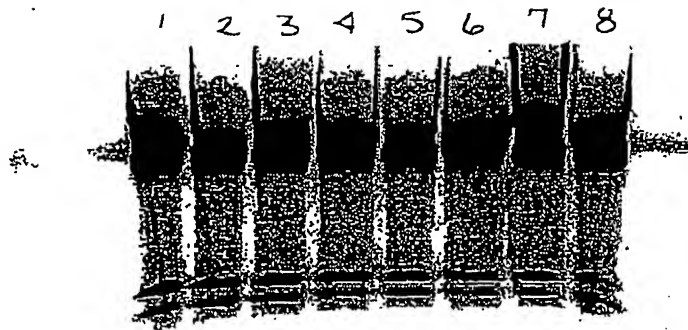


FIGURE 50

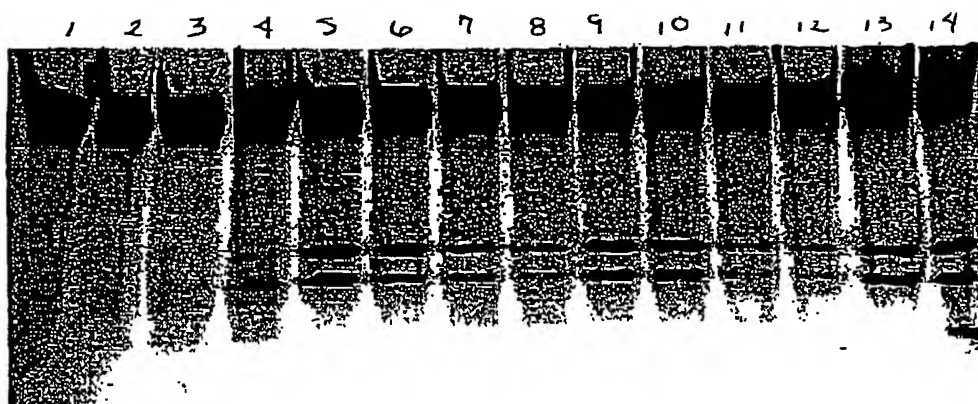


FIGURE 51

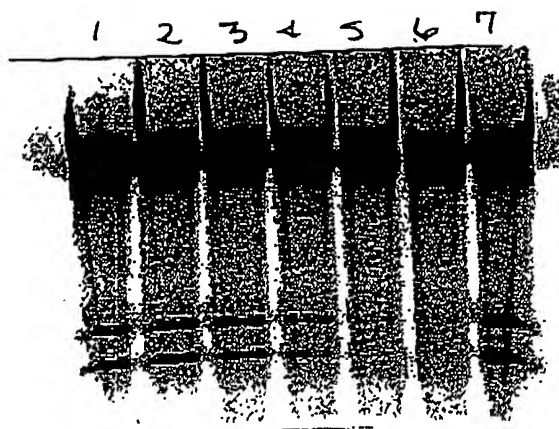


FIGURE 52

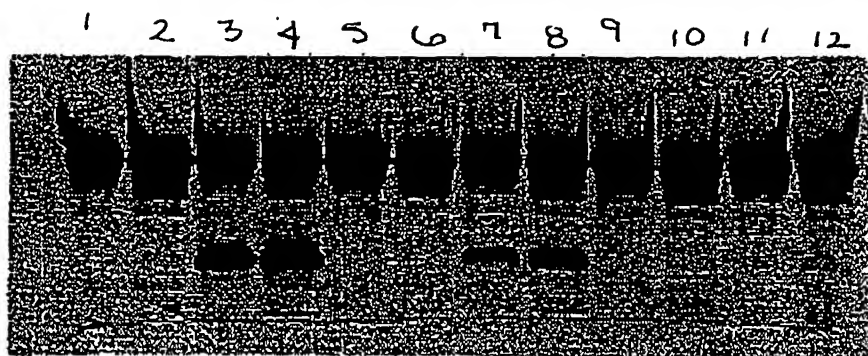


FIGURE 53

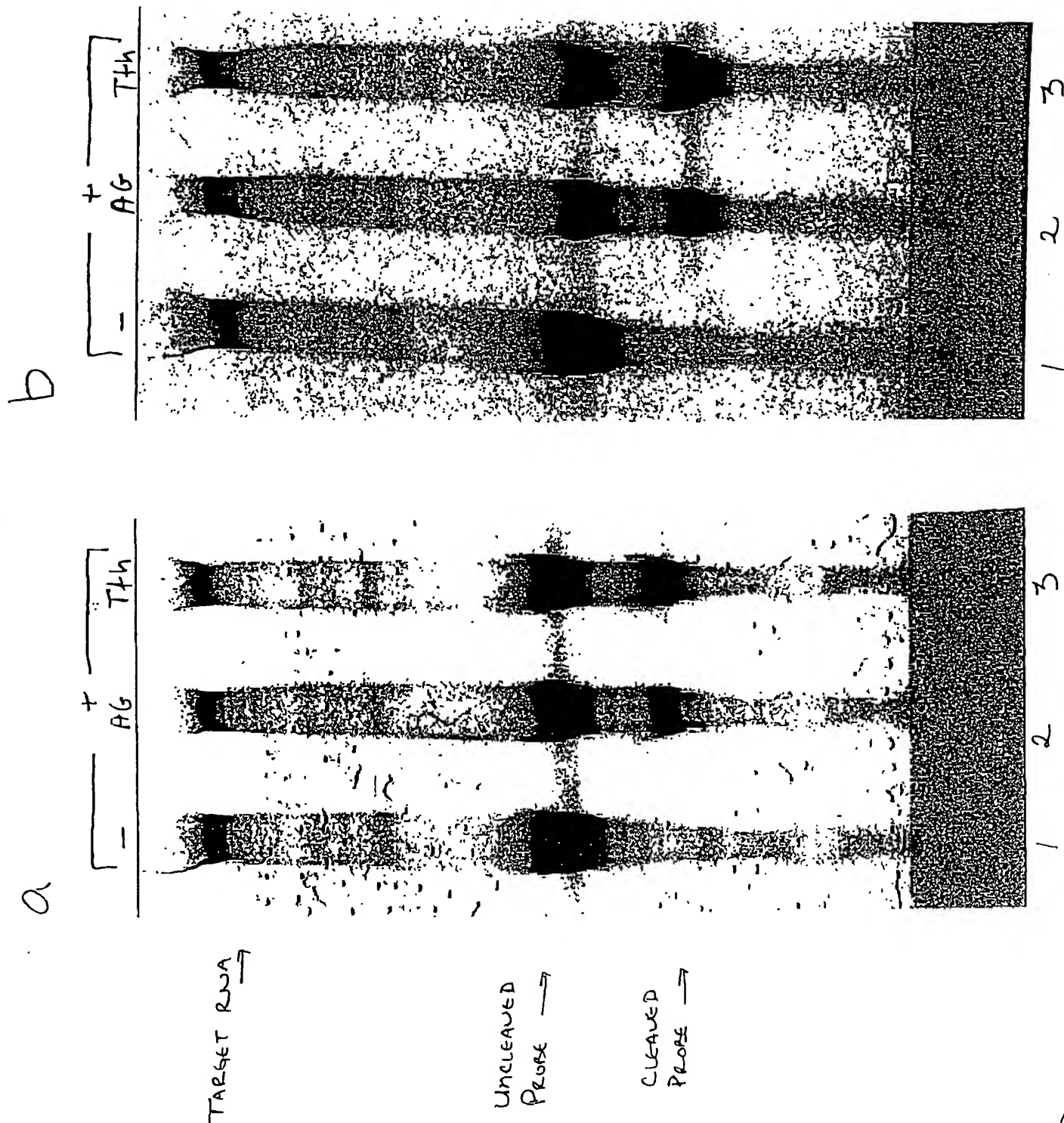


FIGURE 54

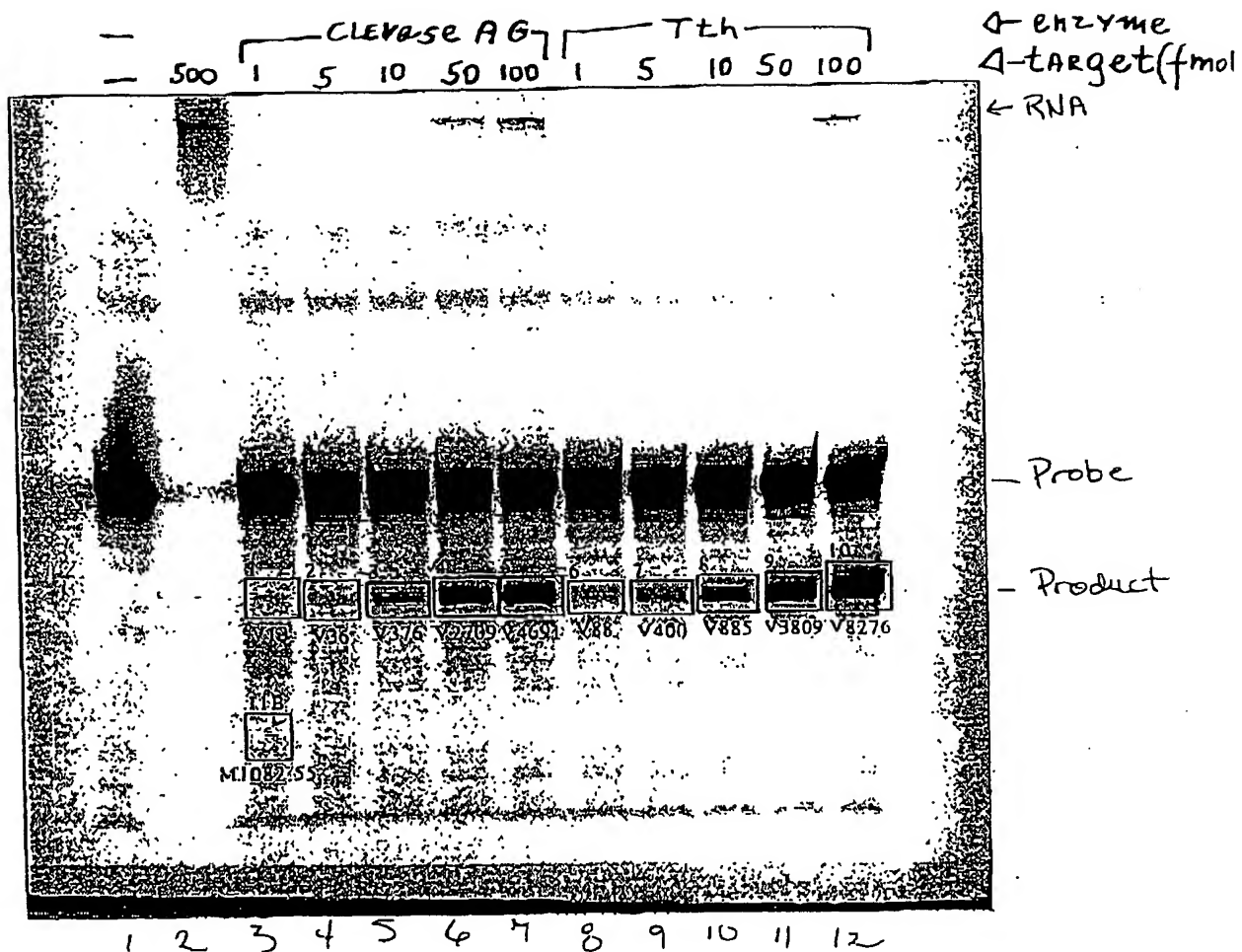


FIGURE 55

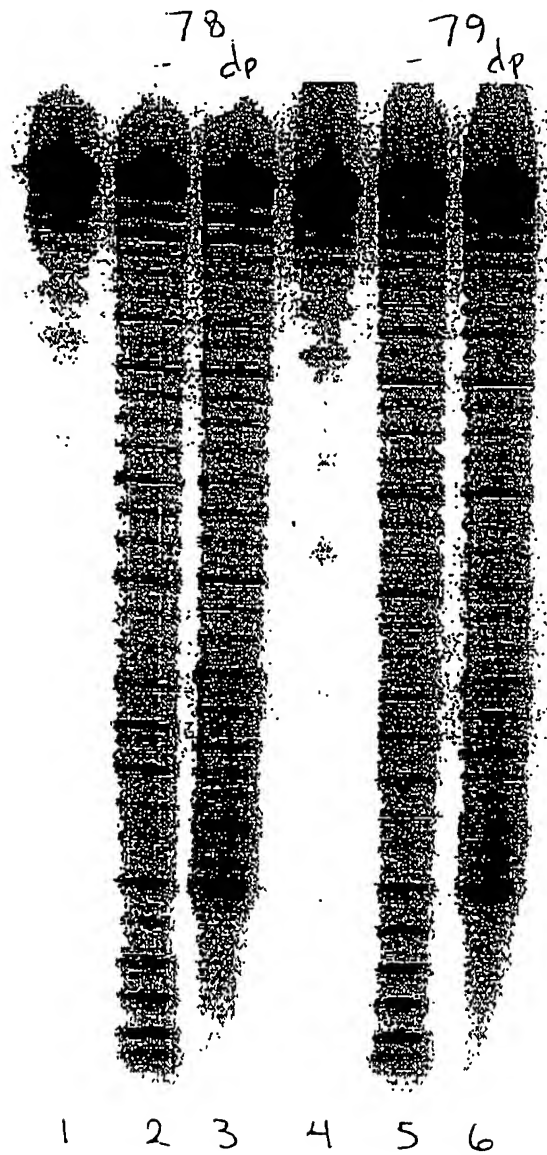


FIGURE 56

70 (C10 aminoT's)

74 (C6 amino T's)

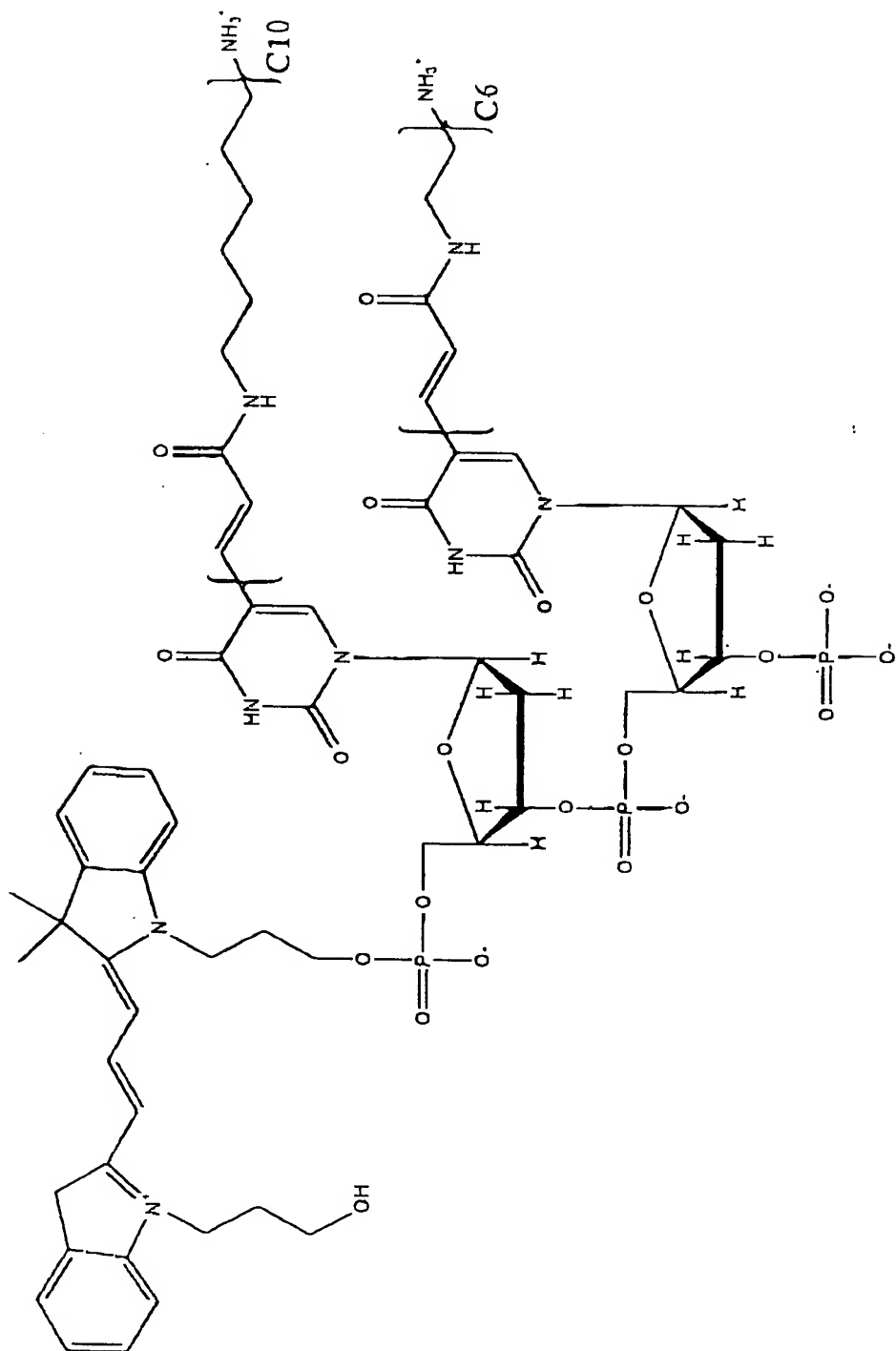


FIGURE 57

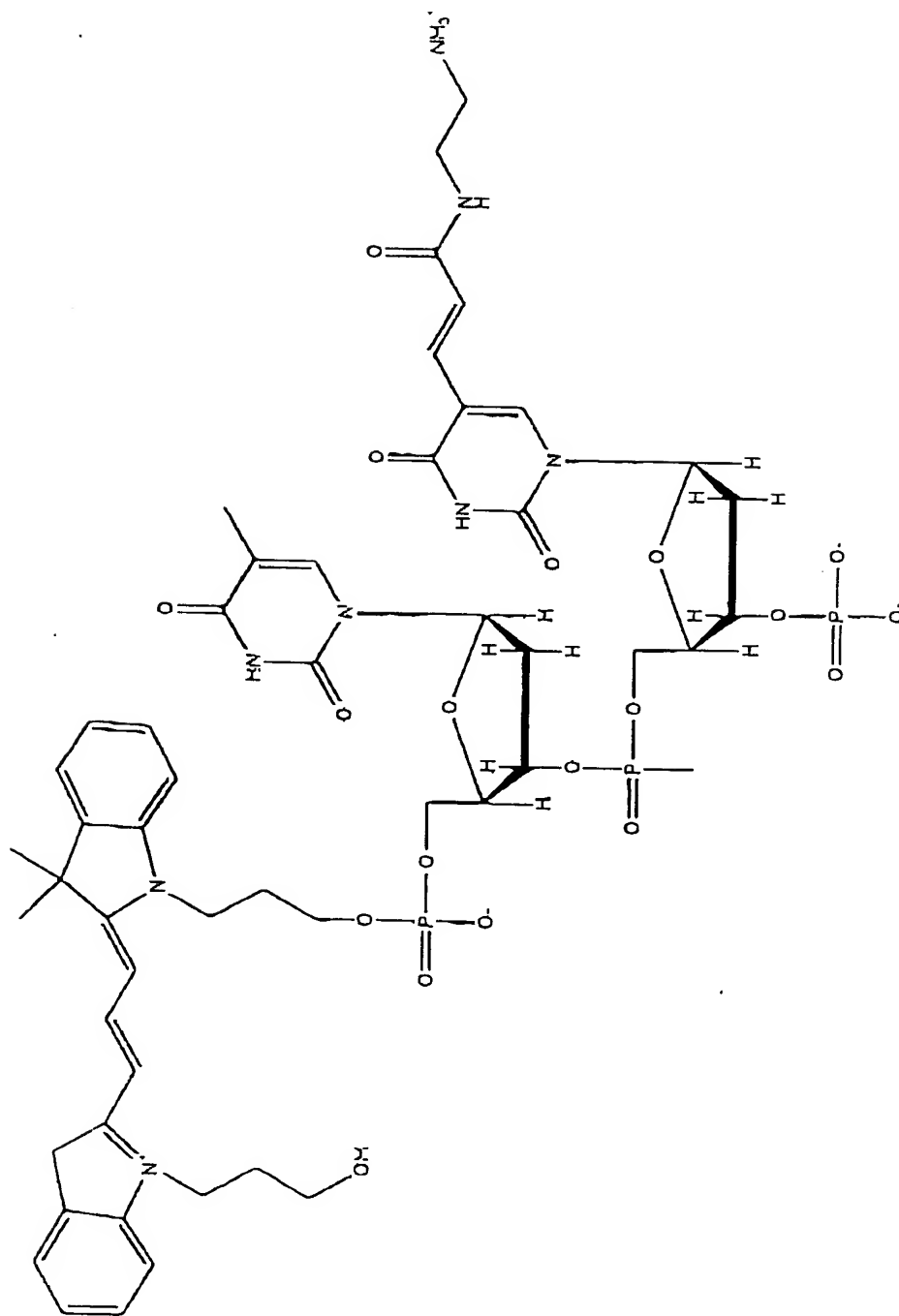


FIGURE 59

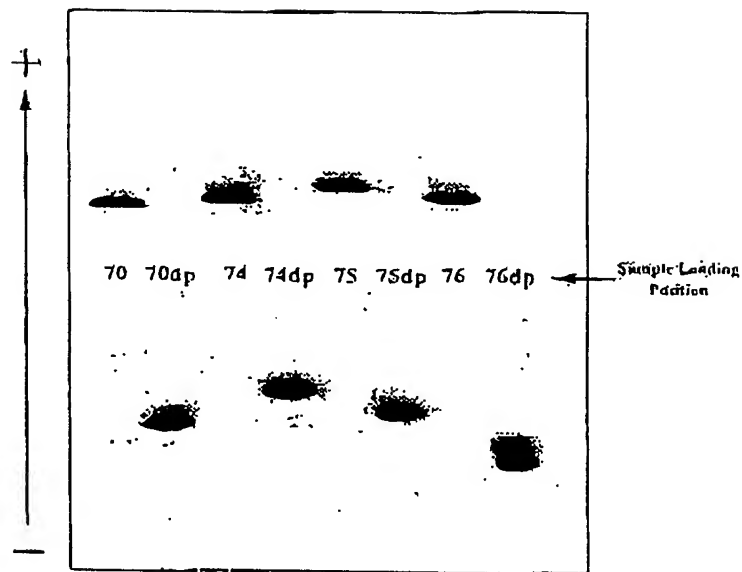
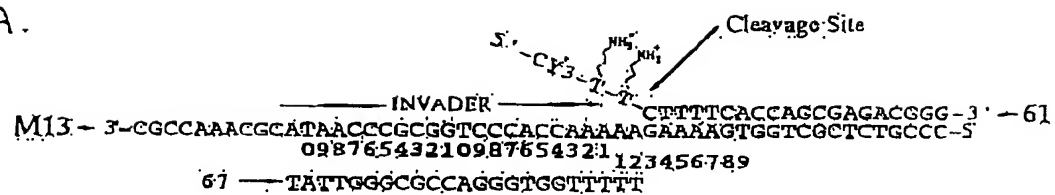


FIGURE 60

A.



B.

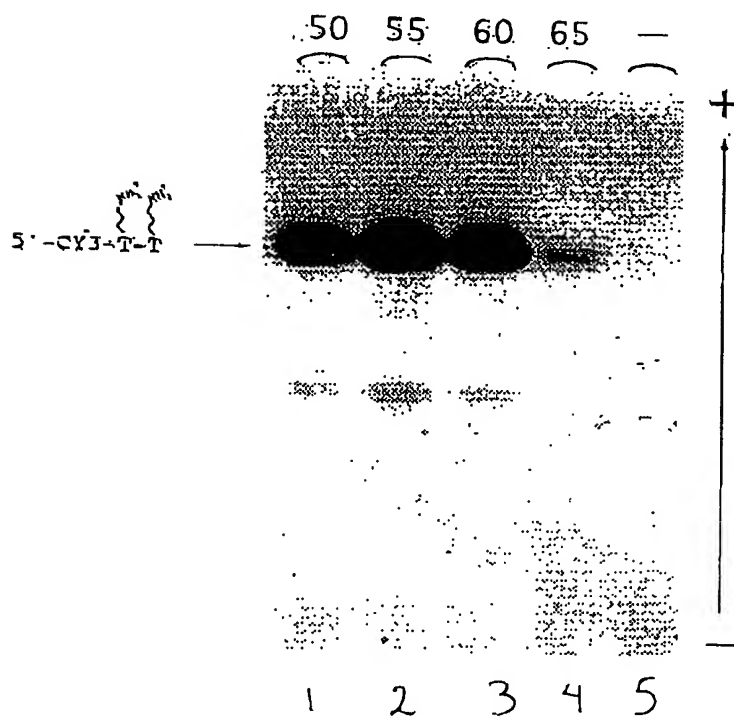


FIGURE 61

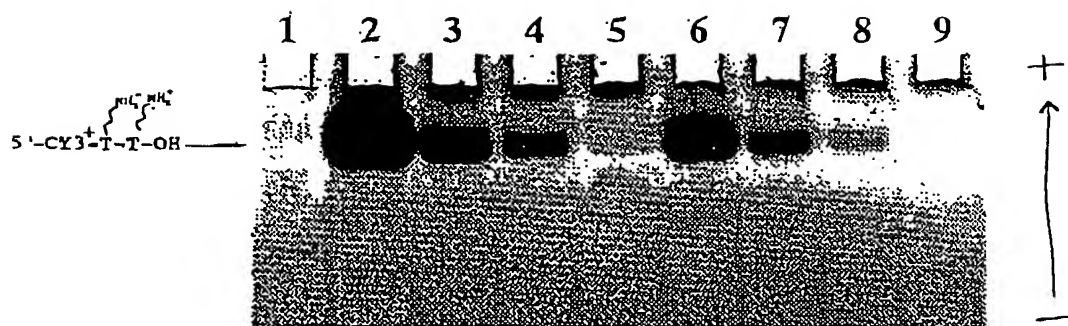


FIGURE 62

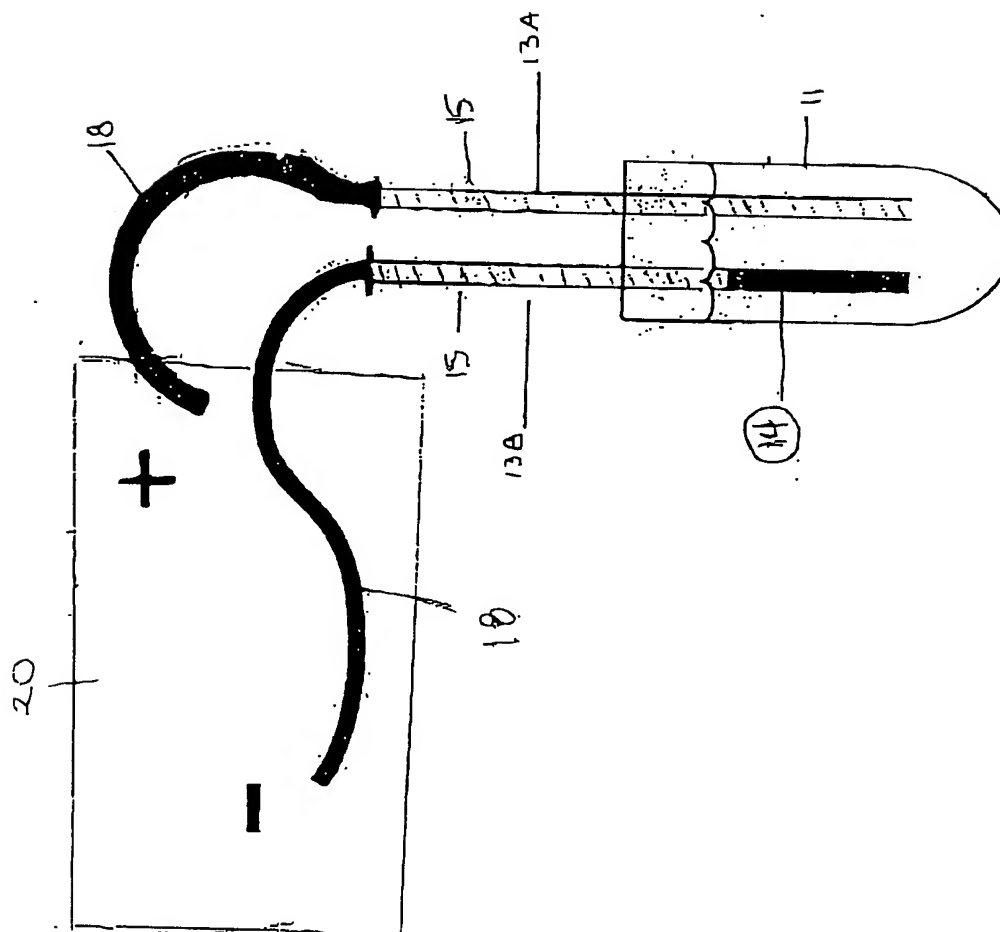


FIGURE 63

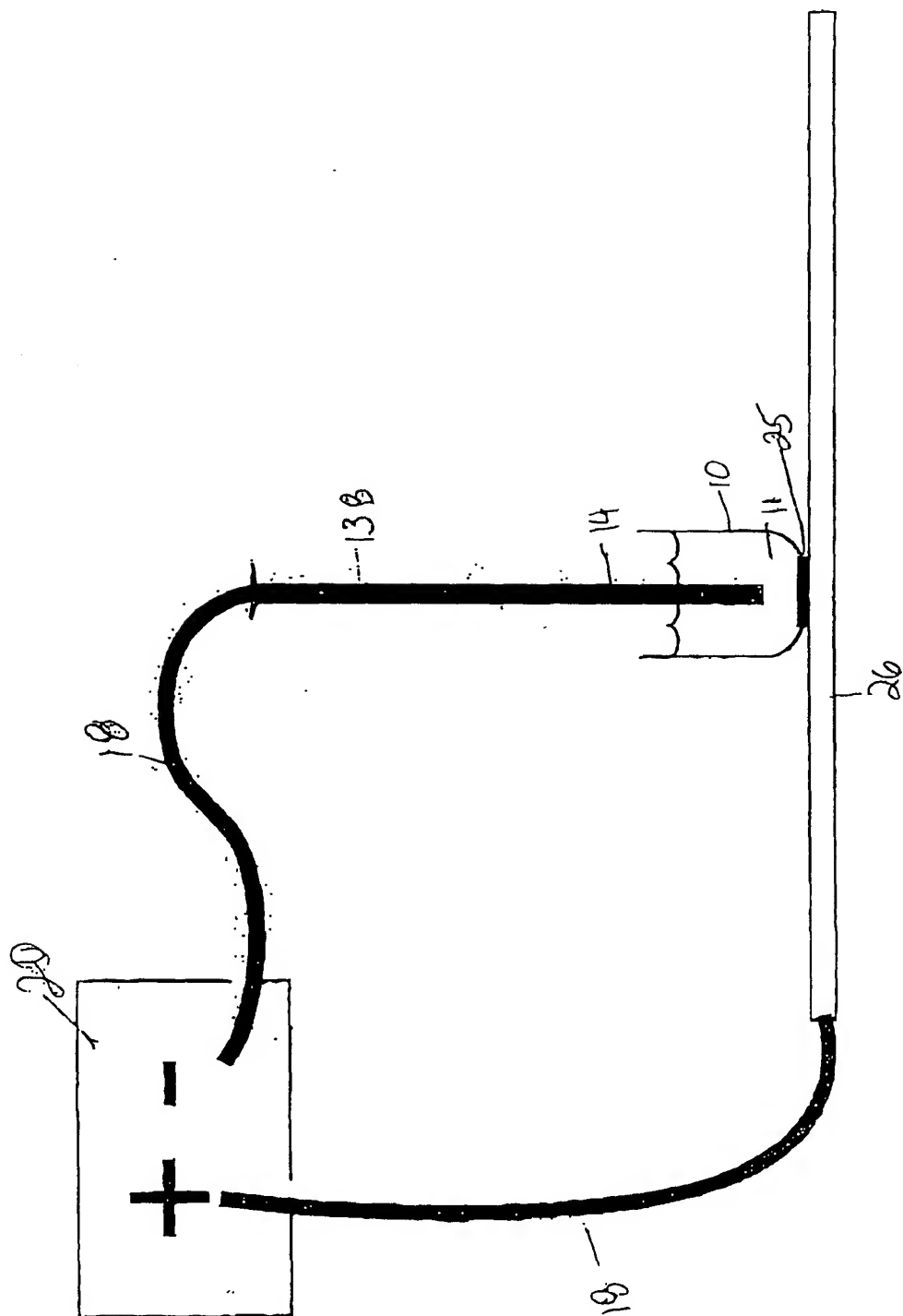


FIGURE 64



FIGURE 65

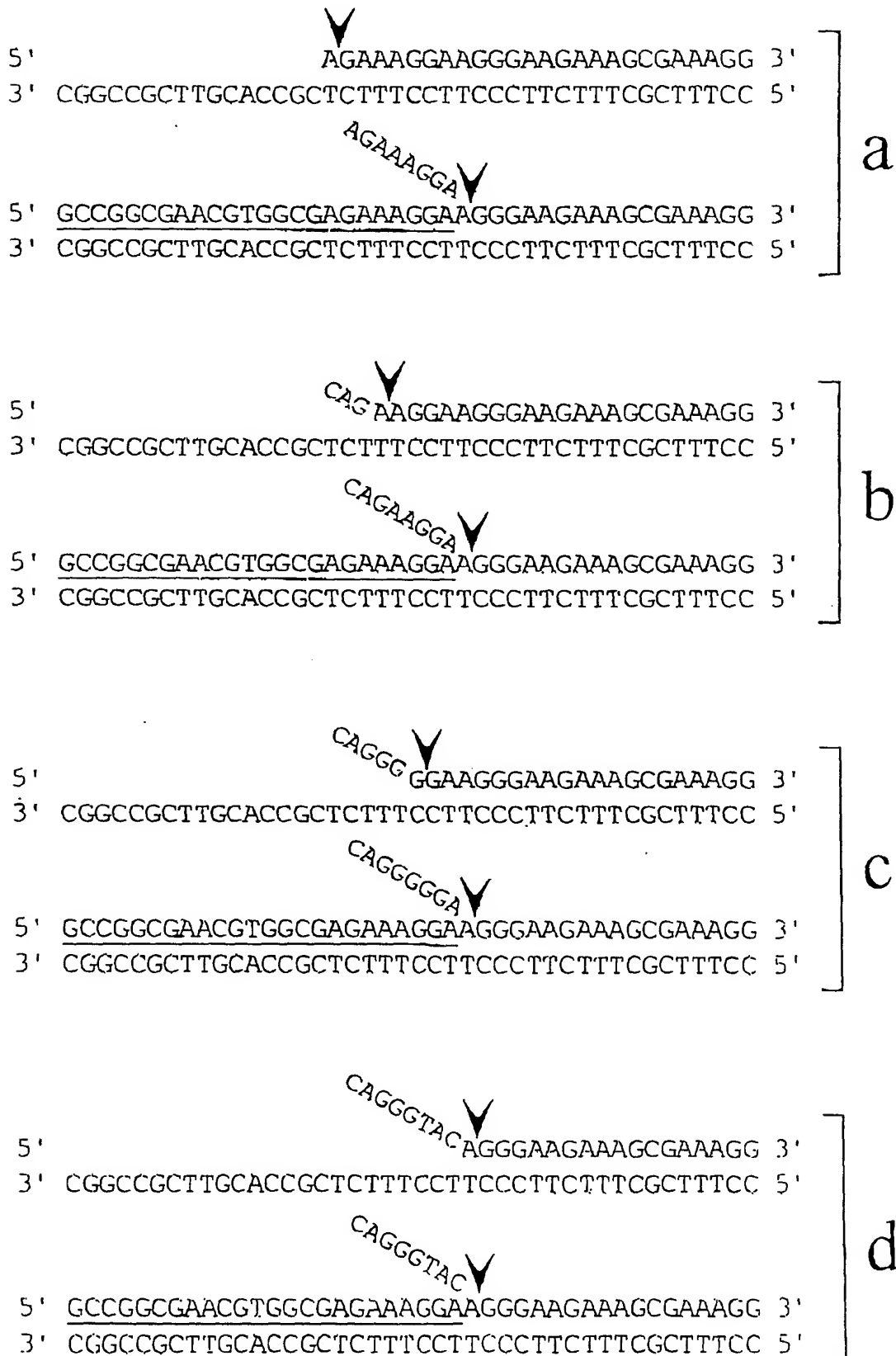


FIGURE 66

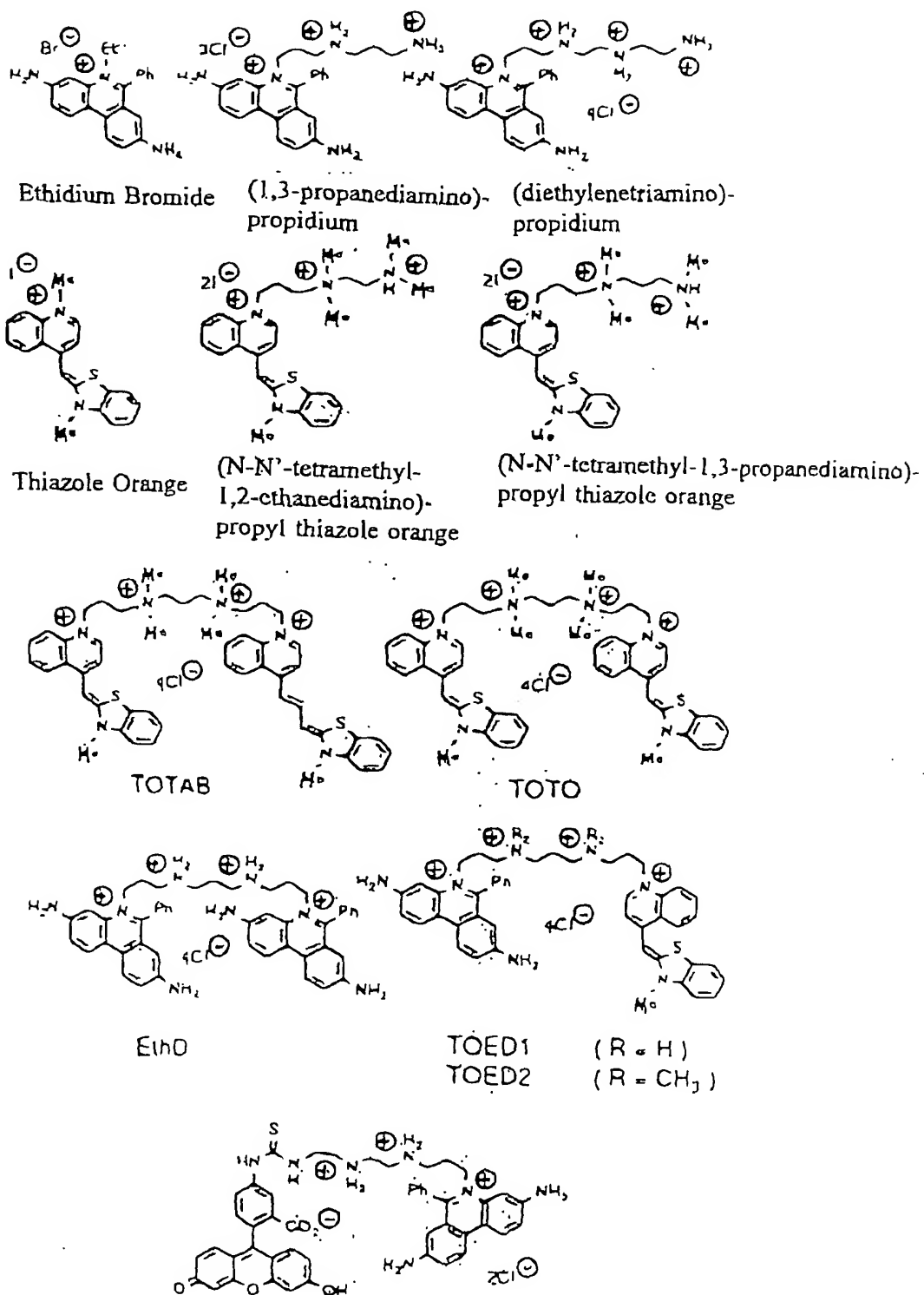


FIGURE 67

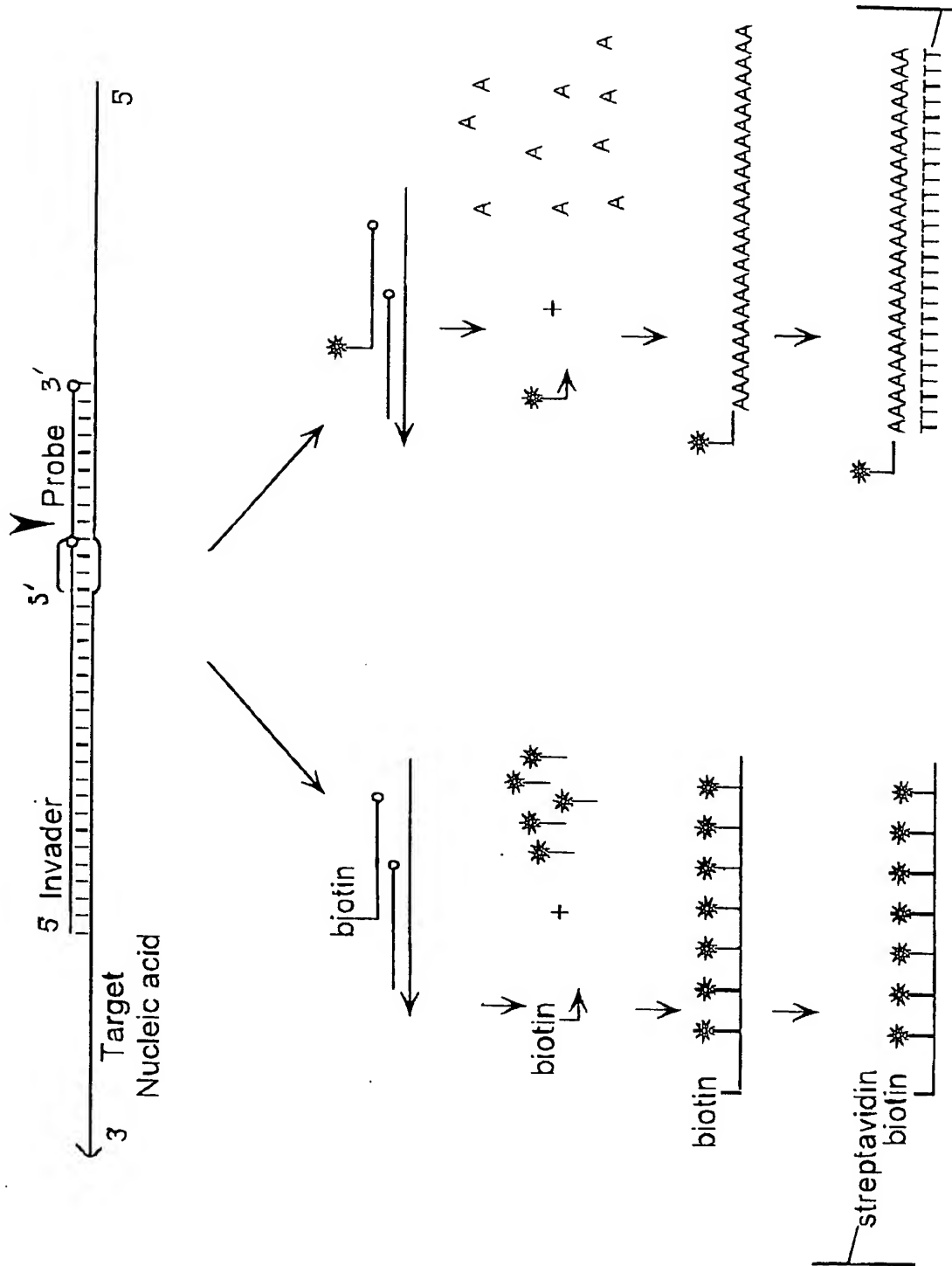


FIGURE 68

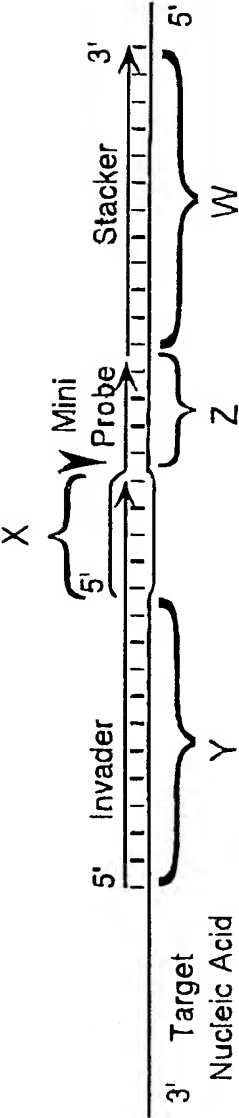


FIGURE 69

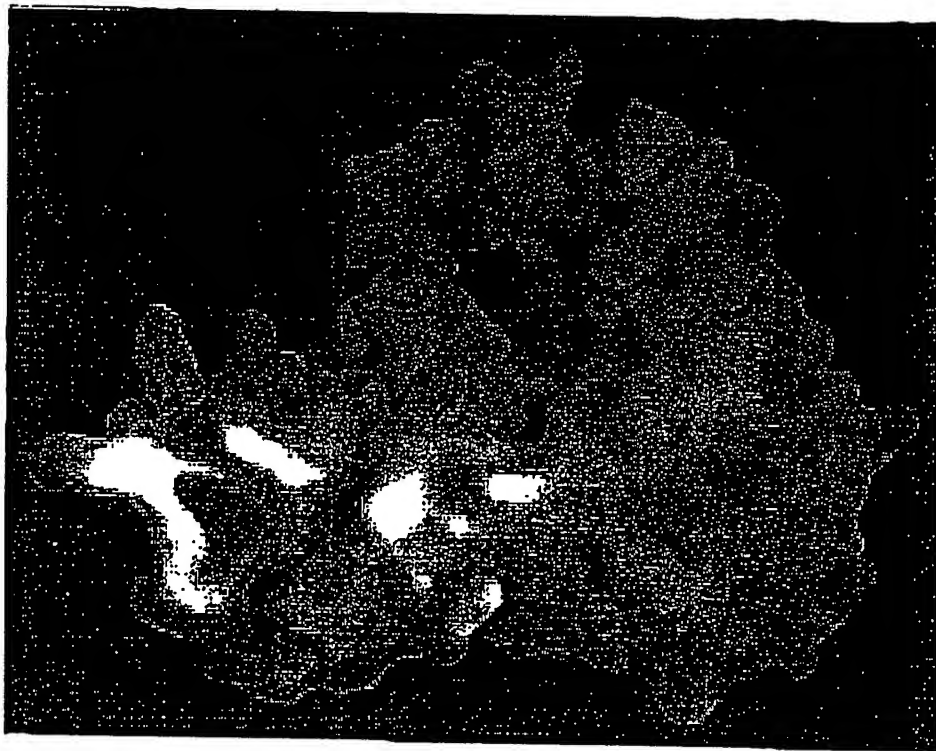


FIGURE 70-A

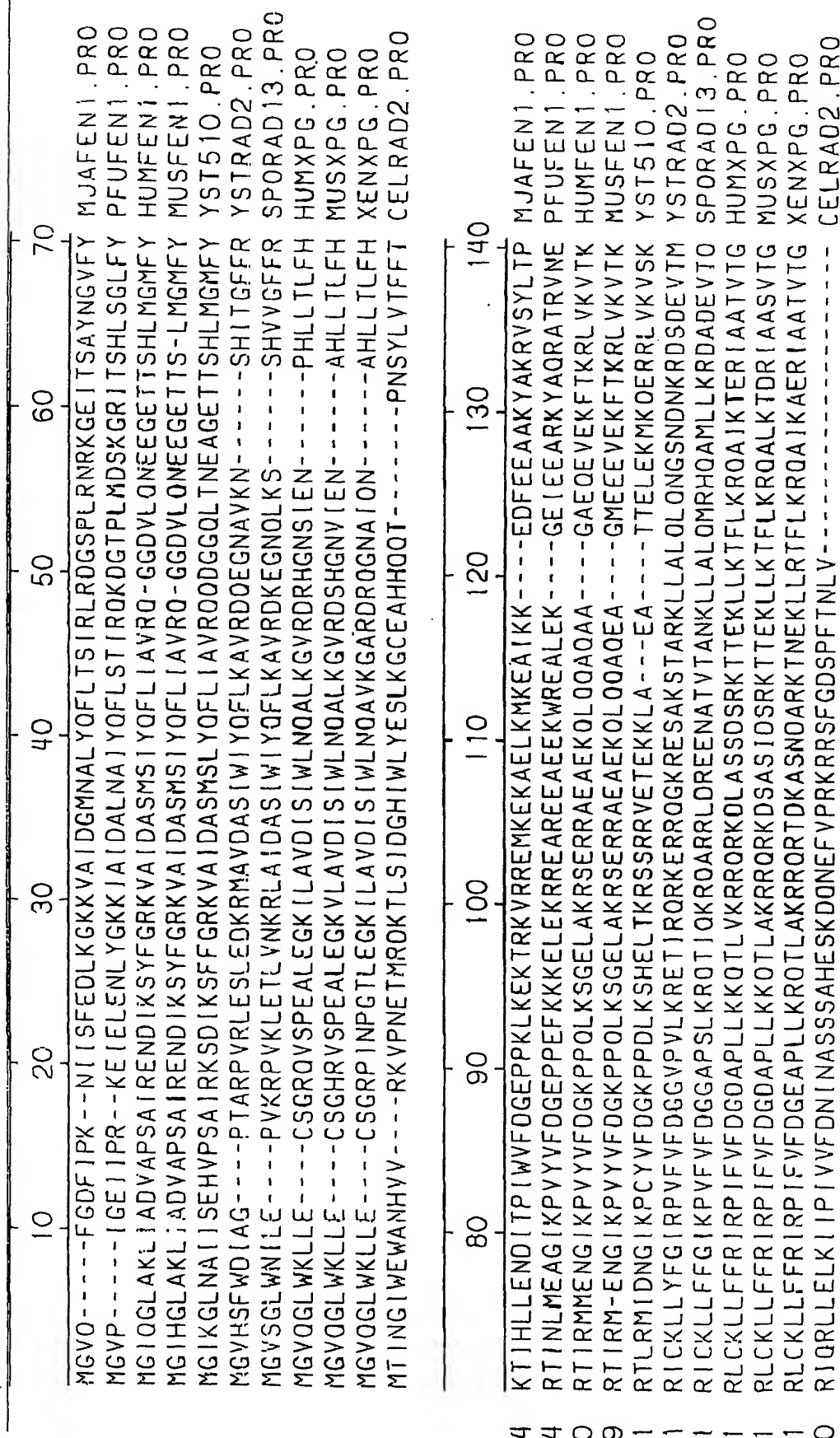


FIGURE 70-B

	150	160	170	180	190	200	210
1130	KMVENCKYLLSLMGIPYVEAPSEGEAQASVMAKKGOVWAVVSOYOALLYGAPRVVRNL	---	---	---	---	---	MJAFEN1.PRO
1130	MLJEDAKKLLLELMGIPYVOAPSEGEAQAAVMAAKGSVYASASQDYDSLFGAPRLVRNL	---	---	---	---	---	PFUFEN1.PRO
1136	QHNOECKHLLSLMGIPYLDAPSEAEASCAALVKAGKVYAAATEDMDCLTFGSPVLMRHL	---	---	---	---	---	TASEAKKLPGK
1134	QHNOECKHLLSLMGIPYLDAPSEAEASCAALAKAGKVYAAATEDMDCLTFGSPVLMRHL	---	---	---	---	---	TASEAKKLPGK
1134	EHNEEAOKLLGLMGIPYIAPTEAEAOCAELAKKGKVYAAASEDMOTLCYRTPFLLRHL	---	---	---	---	---	TFSEAKKEPIH
1131	OMIKEVQELLSRFGIPYITAPMEAEAOCAELLQNLVDGIITDOSOVLFGGTKIYKNMFHEKNY	---	---	---	---	---	VE YSTRAD2.PRO
1131	VMIKECOELLRLFGLPYIVAPQEAEOQCSKLLLEKLVDGIVTDSDYVLFGGTRVYRNMFNONKF	---	---	---	---	---	VE SPORAD13.PRO
1131	QMFLESQELLRLFGIPYIQAPMEAEAOCAILLDLTDQTSGTITDQSDIWLFGARHVYRNFNKNKF	---	---	---	---	---	VE HUMXPG.PRO
1131	QMFLESQELLRLFGVPYIQAPMEAEAOCAVLDLSDQTSGTITDQSDIWLFGARHVYKNFFNKNKF	---	---	---	---	---	VE MUSXPG.PRO
1131	QMCLESQELLRLFGIPYIVAPMEAEAOCAILLDLTDQTSGTITDQSDIWLFGARHVYKNFFSQNHK	---	---	---	---	---	VE XENXPG.PRO
111	DHVYKTNALLTELGIKVIAPGOGEAOCCARLEDLGVTSGCITTDFOYFLFGGKNLYRFDFTAGT	---	---	---	---	---	CELRAD2.PRO

	220	230	240	250	260	270	280
195	-----	PELIELNEVLEDRLISLODLIDIAIFMGTDYNPGGV--K--GIGFKRAYELVRSGVAK--DV					MJAFEN1.PRO
196	-----	NYVE-1KPEL1ILEEVKELKLTREKLIELA1LVGTDYNPGGI--K--GIGLKKALEIVRHSKDPLAKF					PFUFEN1.PRO
197	-----	EFHLSRJLQELGLNOEQVOLCILLGSDYCESIRGIGPKRAVDLIQK--HKSIEEIVRRLOPN----					KY HUFEN1.PRO
198	-----	EFHLSRVLOELGLNOEQVOLCILLGSDYCESIRGIGAKRAVDLIQK--HKSIEEIVRRLOPN----					KY MUSFEN1.PRO
199	-----	EIDTELVRGLDL7IEQFVOLCIMLGCDYCESIRGVGPVTALKIJKT--HGSIEKIVEFIESGESNNTKW					YST510.PRO
200	-----	FYDAESILKLLGLDRKNMIELAQLLGSDYTNGLKGMGPVSSIEVJAEF--GNLKNFKDWNNGOFOKRK					YSTRAD2.PRO
201	-----	LYLMDDMKREFNVNOMDLIKLAHLLGSDYTMGLSRVGPVLALEILHEFFPGDTGLFEFKKWFQRLSTGHAS					SPORAD13.PRO
202	-----	YYQYVDFHNLGLDRNKLINLAYLLGSDYTEGIP TVGCVTAMEILNEFPGHGLEPLLKFSEWWHEAQKNP					HUMXPG.PRO
203	-----	YYQYVDFYSOLGLDRNKLINLAYLLGSDYTEGIP TVGCVTAMEILNEFPGRGLDPLLKFSEWWHEAQNNK					MUSXPG.PRO
204	-----	YYOYAD1HNOLGLDRSKLINLAYLLGSDYTEGIP TVGYVVSAMEILNEFPGOGLEPLVKFEKWSEAOXDK					XENXPG.PRO
205	-----	-----SSTACLDHIMHLSLGRMF-----					CELRAD2.PRO

FIGURE 70-D

	430	440	450	460	470	480	490
314	-	-	-	-	-	-	MJAFEN1.PRO
327	-	-	-	-	-	-	PFUFEN1.PRO
348	-	-	-	-	-	-GSL	HUMFEN1.PRO
346	-	-	-	-	-	-GSL	MUSFEN1.PRO
351	-	-	-	-	-	-PK-T	YST510.PRO
357	KRINEFF	-	-	-	-	-	YSTRAD2.PRO
3359	SNLT OFFEGGNTNVYAPRVAYHFKSKRL	ENALSSFKNO	I SNOSP	MSEE	IQADA	OAFGESKGSDE	LQSRIL SPORAD13.PRO
406	EKEFELLOKAKRKTKRGITNTLEE	SSLKRRLSOSKR	KNTCGGLGETCL	SESSD	GSSSEHAESSLM	HUMXPG.PRO	
406	EKEFELLODAKGKTOKRELPYK	- - - -	-KETSVPKRRRP	SGNGGFLGDPYC	SESPOESSCEDGE	GSSVM MUSXPG.PRO	
403	ERECTNORKGOKTNTKS	- - - -	-OGTKRRRKPT	ECSDQEDQDPGGFI	GIELKTLSSKAYS	S90 - - - - XENXPG.PRO	
3322	MKECGWPATRTOKELALSIRRKVHL	TTTVAQTRIP	OFFAATKSKNF	TPIVEPCESLEDY	ISANN-	- - - - T CELRAD2.PRO	

	500	510	520	530	540	550	560
3314	-----	-----	-----	-----	-----	NKTKOKTL	MJAFEN1.PRO
3327	-----	-----	-----	-----	-----	KSGKOSTL	PFUFEN1.PRO
3352	SAKRKEPEPKGST	-----	-----	-----	-----	KKKAKTGAAG	HUMFEN1.PRO
3350	SAKRKEPEPKGPA	-----	-----	-----	-----	KKKAKTGGAG	MUSFEN1.PRO
3354	KEGLAAAARAQE	-----	-----	-----	-----	NKKLNKNKNK	YST510.PRO
3364	-----	-----	PREYISGDKKLNTSKRISTATGKL	-----	-----	-----	YSTRAD2.PRO
4129	RRKXMMASKNSSDSCDSEDNFLASLTPKTNSSSISLENLPRKTKLSTSL	-----	-----	-----	-----	-----	SPORAD13.PRO
4476	NVORRTAAKEPKTSASDSONSVKEAPVKNGGATTSSSSDSDGGKEKMYLVTARSVFGKKRRKLRARG	-----	-----	-----	-----	-----	HUMXPG.PRO
4469	SARQRSAAESSKIGCSOVPDLVROSPHGRQGCVSTSSDSEDGEOKAKTVLVTARPVFGKKRRKLSMK	-----	-----	-----	-----	-----	MUSXPG.PRO
4458	-----	GSSSDAEDLPSGLIDKOSOSGIVGROKASNKVESSSSDSEDRTVMVTAKPVFGKKTKSKTMKE	-----	-----	-----	-----	XENXPG.PRO
3387	WMRKRRKRSPOILQHHAKRQVPORK	-----	-----	-----	-----	RSVKIRAFKPYPTOVJ	CELRAO2.PRO

85 ✓

FIGURE 70-E

22 DAWFKZ
35 ESWFKR
75 KFKRGK
73 KFRRGK
77 VTKGRR
90 ---RKM
83 SKRRRK
46 RKRK TZ
38 RRKKKT
23 TVKRK
29 ELGDSD

MJAFEN1.PRO
PFUFEN1.PRO
HUMFEN1.PRO
MUSFEN1.PRO
YST510.PRO
YSTRAD2.PRO
SPORAD13.PRO
HUMXPG.PRO
MUSXPG.PRO
XENXPG.PRO
CELRAD2.PRO

FIGURE 71

